

FIG.1

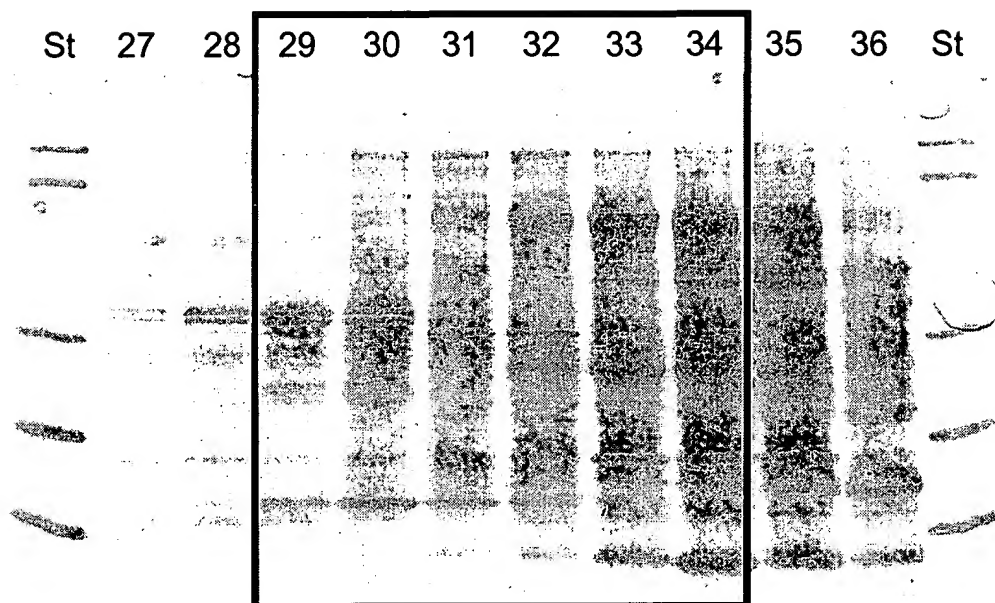


FIG.2

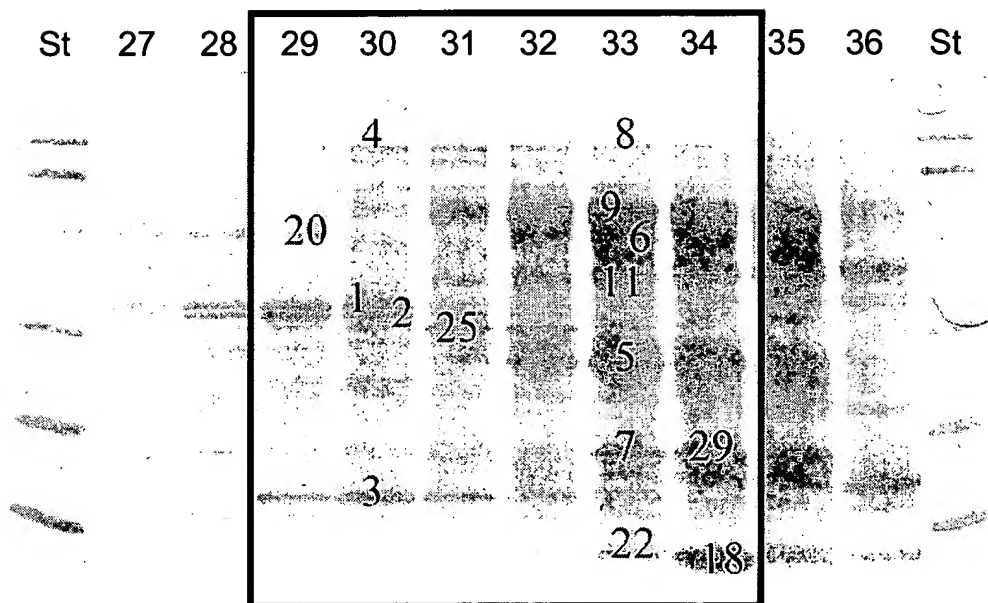
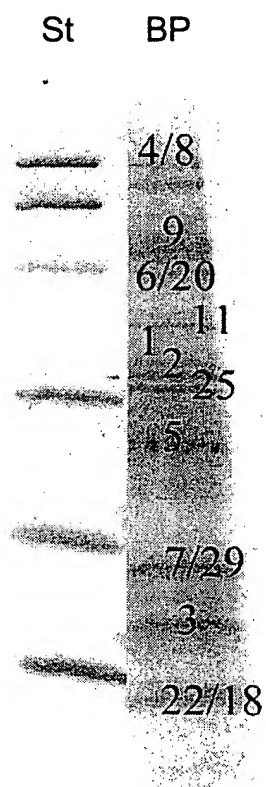


FIG.3



BAND NO.	IDENTITY
1	HISTONE H1.c
2	HISTONE H1.c
3	RIBOSOMAL PROTEIN RS20
4	SIMILAR TO RIBOSOMAL PROTEIN LORP
5	BMP-3
6	α 2 MACROGLOBULIN RAP AND BMP-3
7	SIMILAR TO RIBOSOMAL PROTEIN LORP
8	BMP-3
9	BMP-3
11	RIBOSOMAL PROTEIN RL6 AND BMP-3
18	TGF- β 2/SPP 24
20	FACTOR H
22	TGF- β 2
25	BMP-3 AND H1.x
29	BMP-3 AND RIBOSOMAL PROTEIN RL32

FIG.4

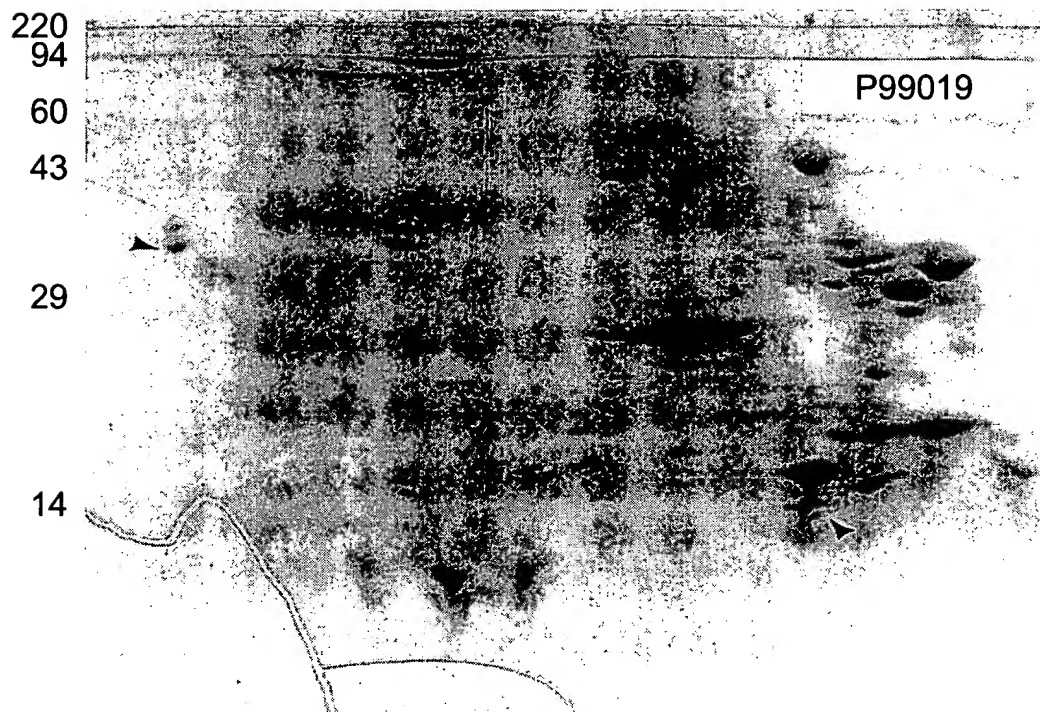


FIG.5

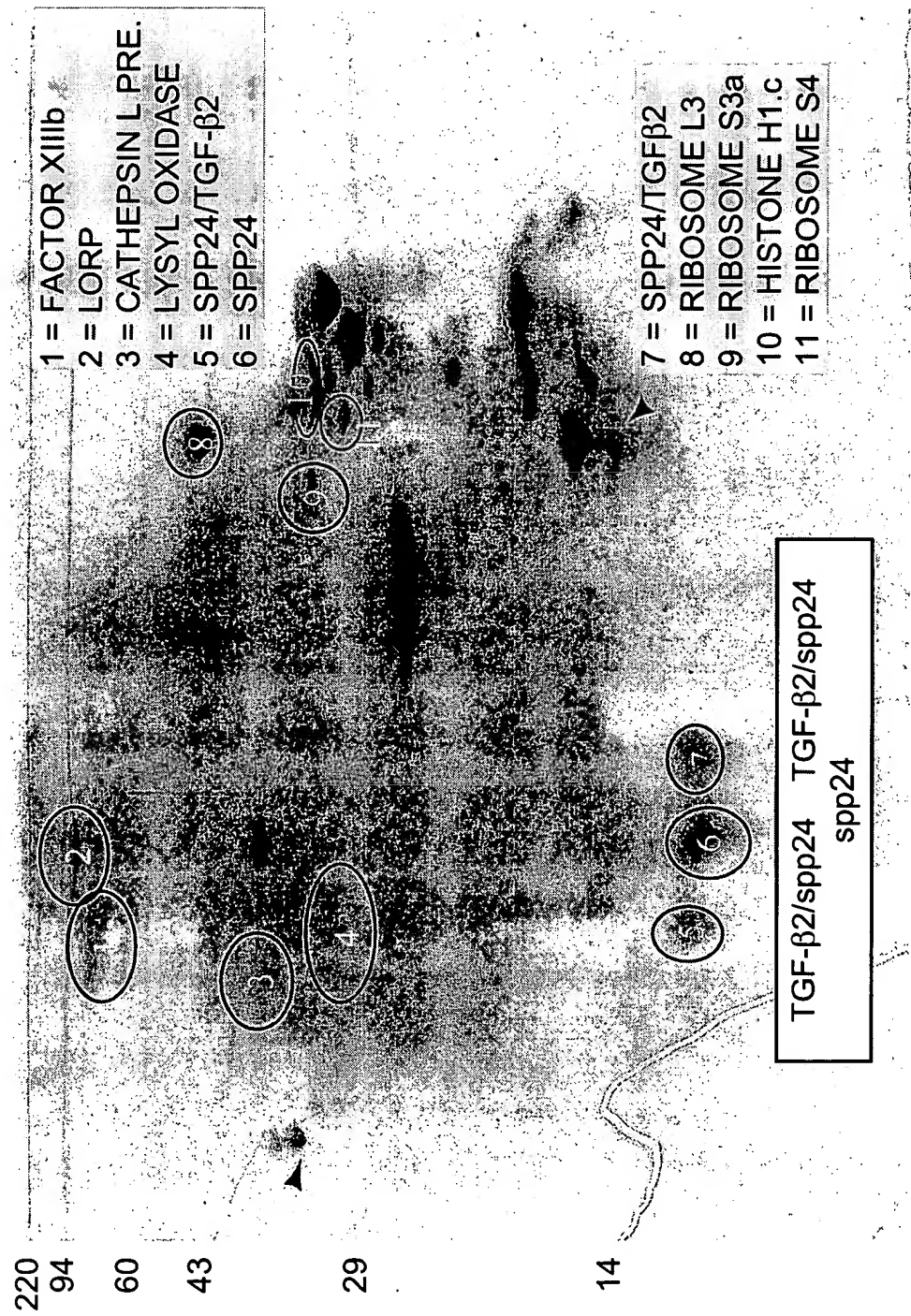
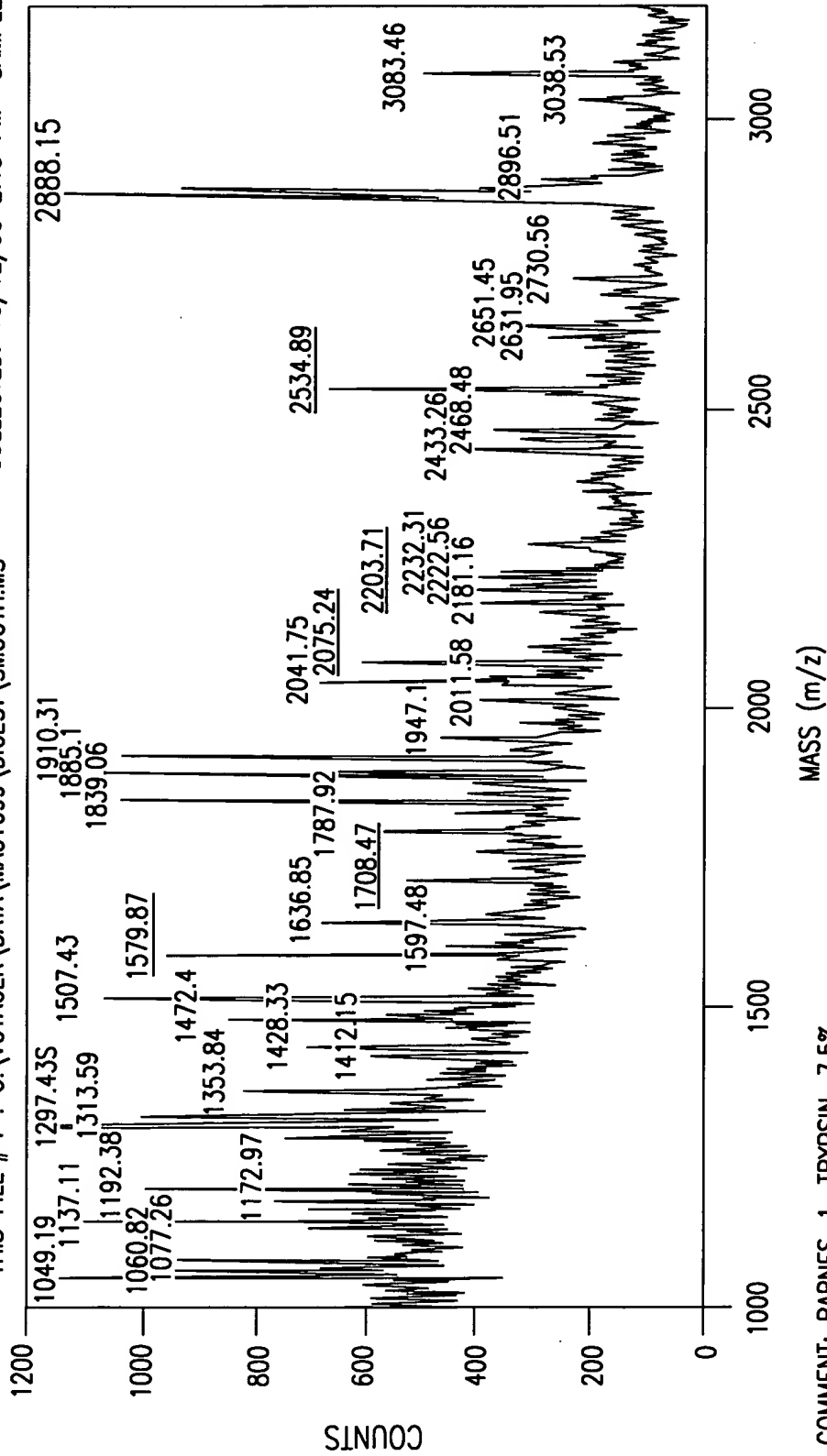


FIG.6

ORIGINAL FILENAME: c:\voyager\data\mag1099\digest\barne026.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
THIS FILE # 1 : C:\VOYAGER\DATA\MAG1099\DIGEST\SMOOTH.MS COLLECTED: 10/12/99 2:13 PM SAMPLE: 74



COMMENT: BARNES-1, TRYPSIN, 7.5%

METHOD: LDE1000A

MODE: LINEAR

ACCELERATING VOLTAGE: 20000

GRID VOLTAGE: 94.000%

GUIDE WIRE VOLTAGE: 0.075%

DELAY: 50 ON

LASER: 1965

SCANS AVERAGED: 256

PRESSURE: 1.70e-06

LOW MASS GATE: 500.0

MIRROR RATIO: 1.060

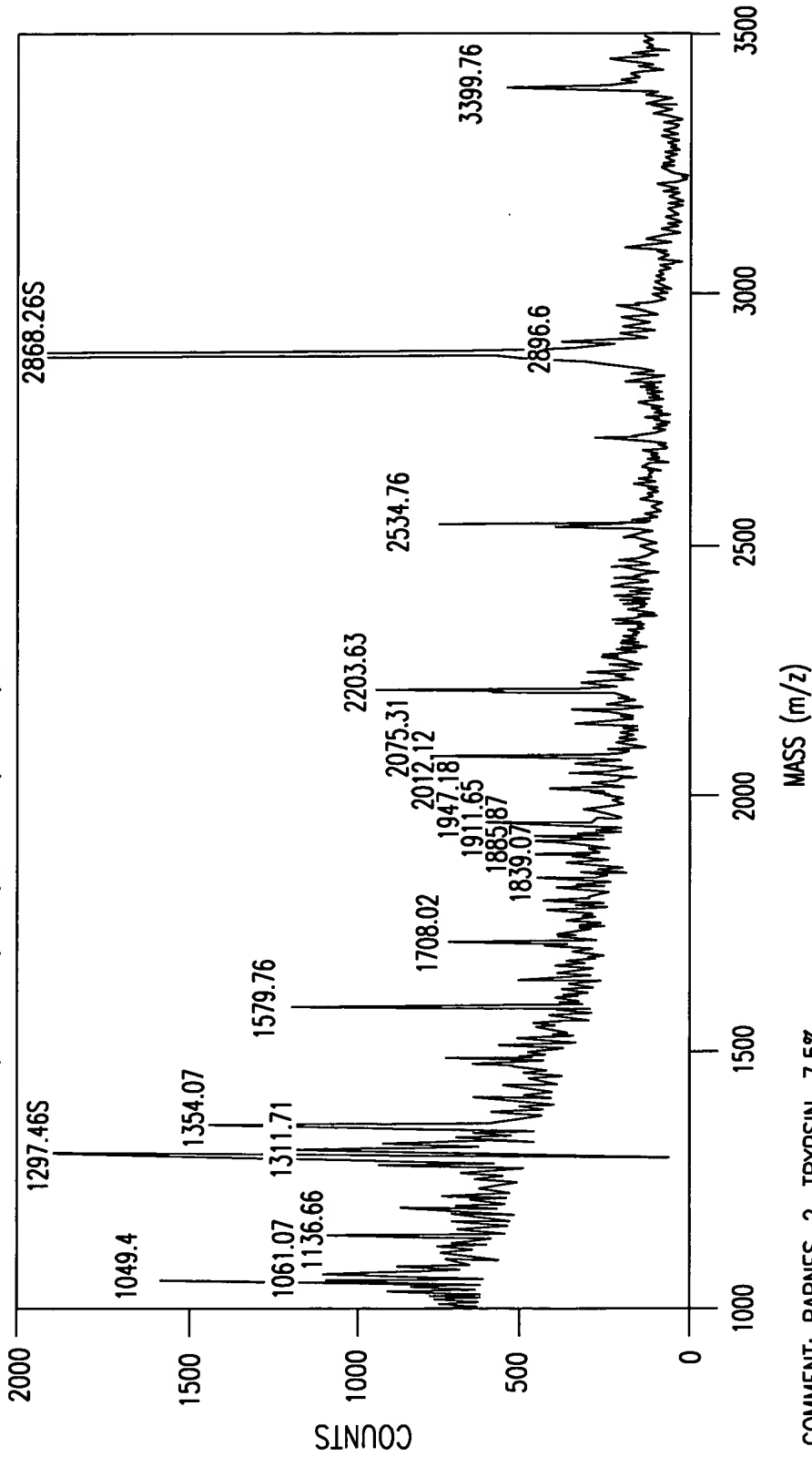
PSD MIRROR RATIO:

TIMED ION SELECTOR: 16.1 OFF

NEGATIVE IONS: OFF

FIG.7A

ORIGINAL FILENAME: c:\voyager\data\mag1099\digest\barne027.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
 THIS FILE # 1 : C:\VOYAGER\DATA\MAG1099\DIGEST\SMOOTH.MS COLLECTED: 10/12/99 2:21 PM SAMPLE: 75



COMMENT: BARNES-2, TRYPSIN, 7.5%

METHOD: LDE1000A
 MODE: LINEAR

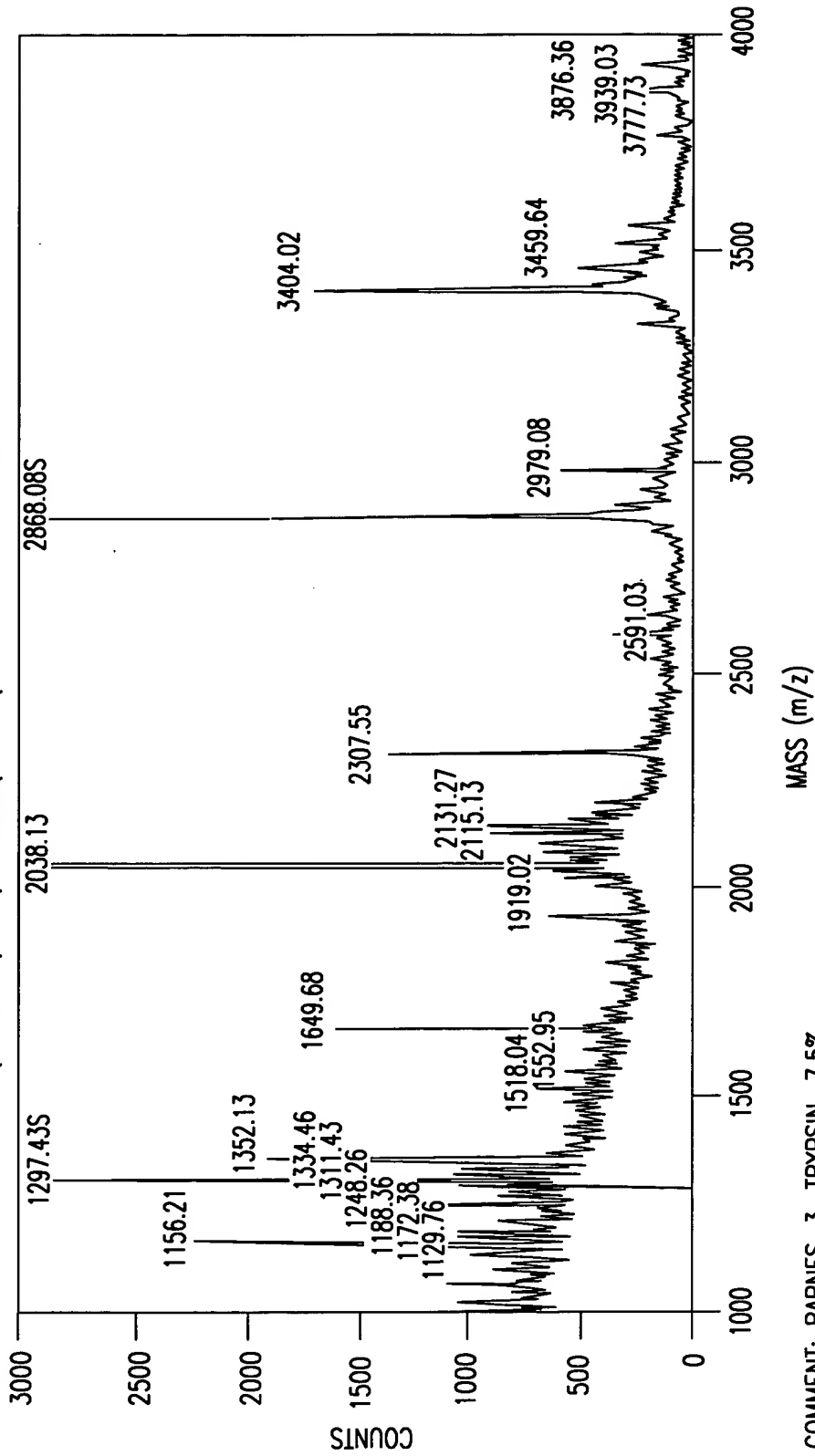
ACCELERATING VOLTAGE: 20000
 GRID VOLTAGE: 94.000%
 GUIDE WIRE VOLTAGE: 0.075%

LASER: 1965
 SCANS AVERAGED: 256
 PRESSURE: 1.58e-06
 LOW MASS GATE: 500.0
 DELAY: 50 ON

MIRROR RATIO: 1.060
 PSD MIRROR RATIO:
 TIMED ION SELECTOR: 16.1 OFF
 NEGATIVE IONS: OFF

FIG.7B

ORIGINAL FILENAME: c:\voyager\data\mag1099\digest\barne028.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
THIS FILE # 1 : C:\VOYAGER\DATA\MAG1099\DIGEST\SMOOTH.MS COLLECTED: 10/12/99 2:31 PM SAMPLE: 76



COMMENT: BARNES-3, TRYPSIN, 7.5%

METHOD: LDE1000A
MODE: LINEAR

ACCELERATING VOLTAGE: 20000
GRID VOLTAGE: 94.000%
GUIDE WIRE VOLTAGE: 0.075%

LASER: 1965

SCANS AVERAGED: 256
PRESSURE: 1.58e-06
LOW MASS GATE: 500.0

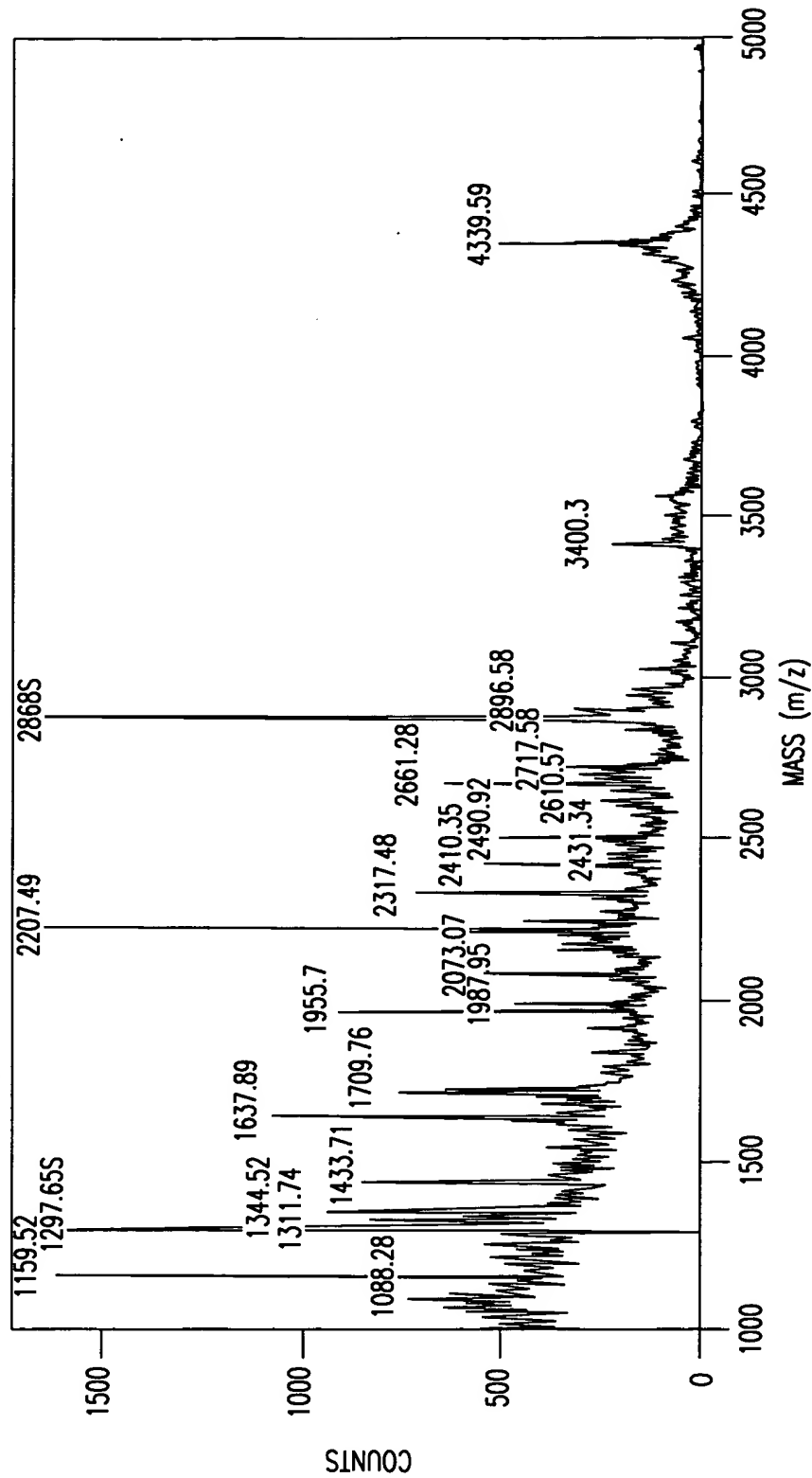
MIRROR RATIO: 1.060

PSD MIRROR RATIO:

TIMED ION SELECTOR: 16.1 OFF
NEGATIVE IONS: OFF

FIG.7C

ORIGINAL FILENAME: c:\voyager\data\mag1099\barnes\barne037.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
THIS FILE # 1 : C:\VOYAGER\DATA\MAG1099\BARNES\SMOOTH.MS COLLECTED: 10/27/99 2:30 PM SAMPLE: 22



COMMENT: BARNES-4, TRYS 5%

METHOD: LDE1000A
MODE: LINEAR

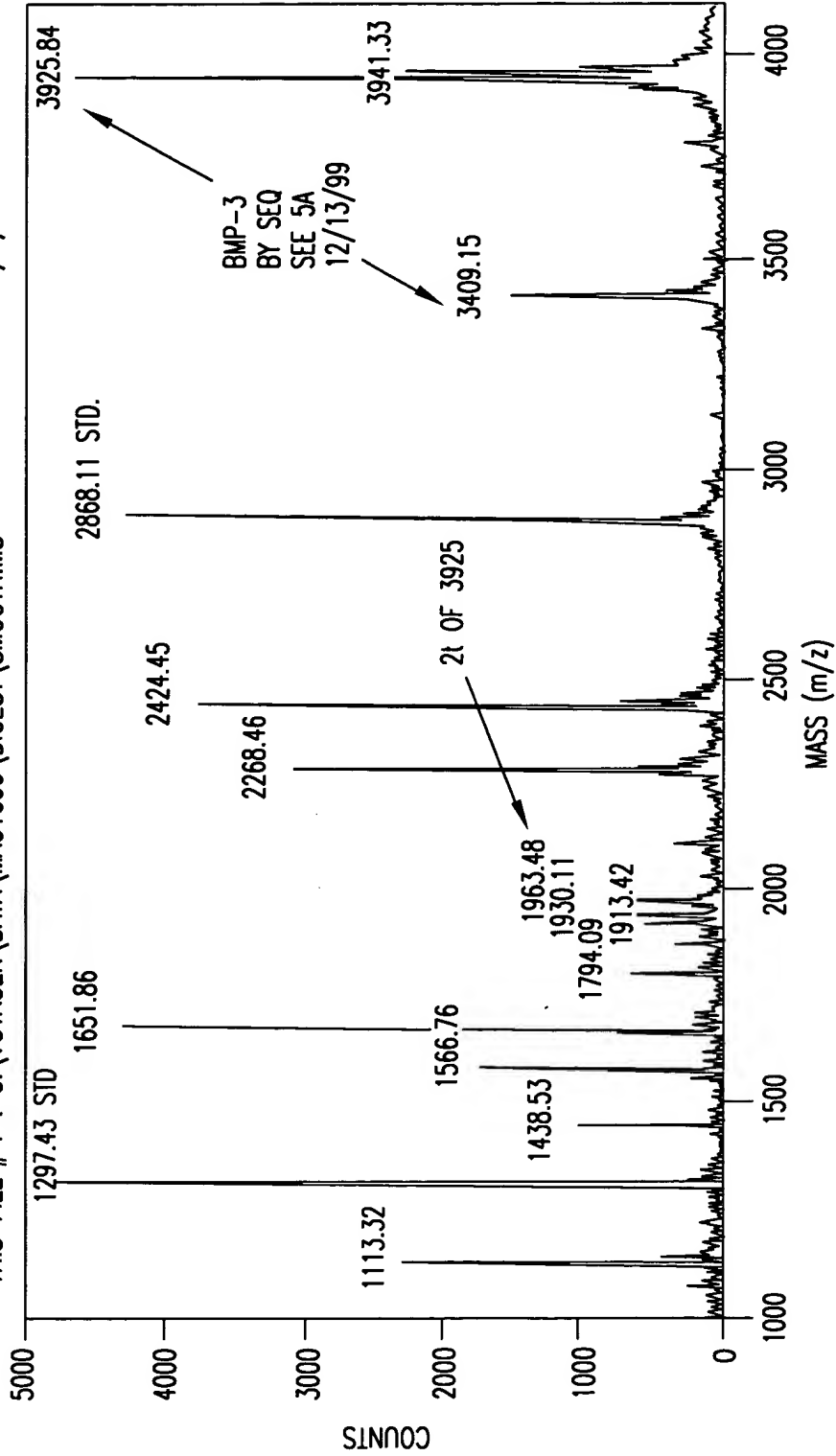
ACCELERATING VOLTAGE: 20000
GRID VOLTAGE: 94.000%
GUIDE WIRE VOLTAGE: 0.075%
DELAY: 50 ON

LASER: 1965
SCANS AVERAGED: 256
PRESSURE: 9.04e-06
LOW MASS GATE: 500.0

MIRROR RATIO: 1.060
PSD MIRROR RATIO:
TIMED ION SELECTOR: 16.1 OFF
NEGATIVE IONS: OFF

FIG.7D

ORIGINAL FILENAME: c:\voyager\data\mag1099\digest\barne02.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
 THIS FILE # 1 : C:\VOYAGER\DATA\MAG1099\DIGEST\SMOOTH.MS COLLECTED: 10/5/99 1:16 PM SAMPLE: 32



COMMENT: BARNES TRYPS #5

METHOD: LDE1000A
 MODE: LINEAR

ACCELERATING VOLTAGE: 20000
 GRID VOLTAGE: 94.000%
 GUIDE WIRE VOLTAGE: 0.075%

LASER: 1965

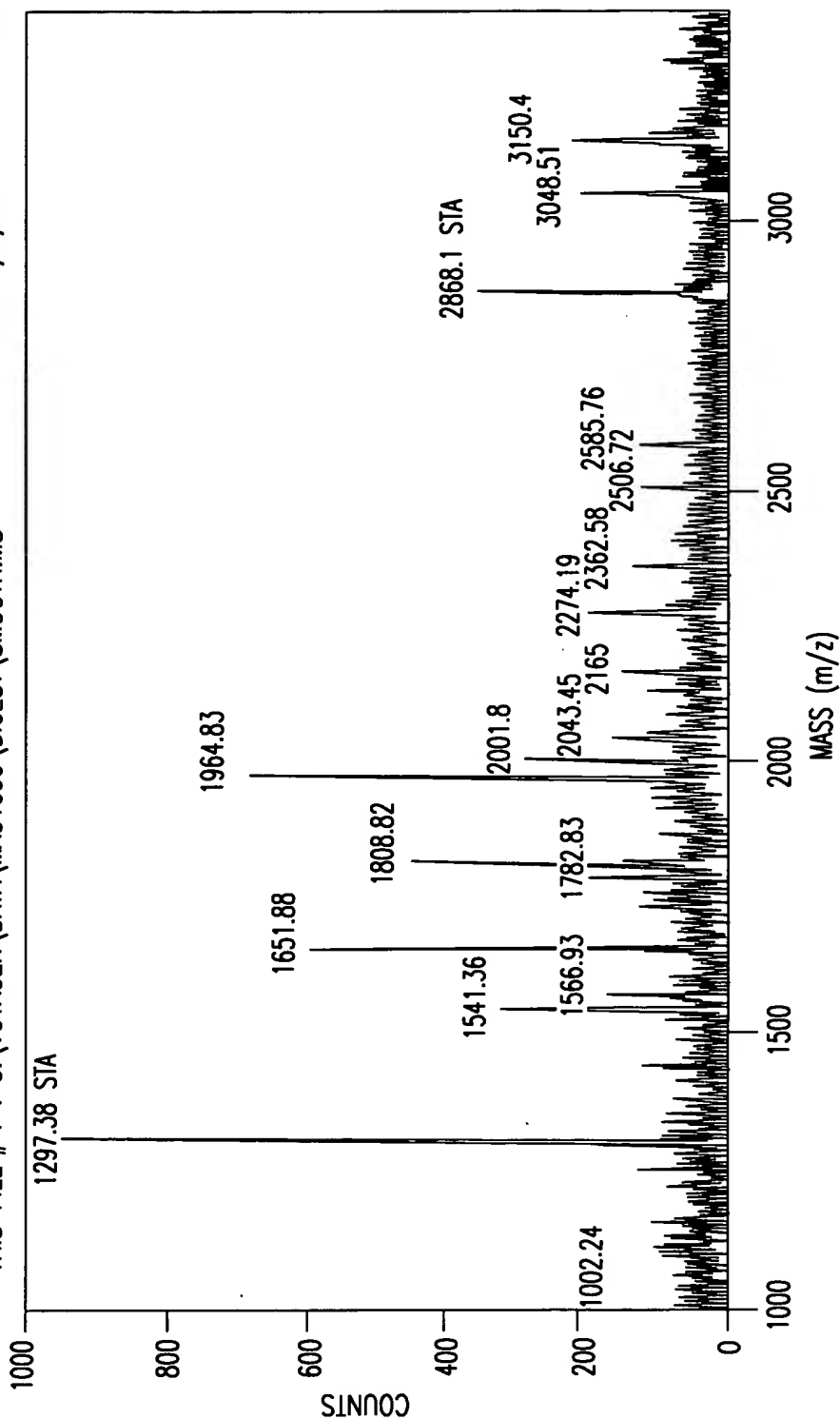
SCANS AVERAGED: 121
 PRESSURE: 3.68e-07
 LOW MASS GATE: 500.0

MIRROR RATIO: 1.060

PSD MIRROR RATIO:
 TIMED ION SELECTOR: 16.1 OFF
 NEGATIVE IONS: OFF

FIG.7E

ORIGINAL FILENAME: c:\voyager\data\mag1099\digest\barne001.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
THIS FILE # 1 : C:\VOYAGER\DATA\MAG1099\DIGEST\SMOOTH.MS COLLECTED: 10/5/99 1:14 PM SAMPLE: 33



COMMENT: BARNES-4, TRYPS #6

METHOD: LDE1000A
MODE: LINEAR

ACCELERATING VOLTAGE: 20000

GRID VOLTAGE: 94.000%

GUIDE WIRE VOLTAGE: 0.075%

DELAY: 50 ON

LASER: 1965

SCANS AVERAGED: 256

PRESSURE: 4.06e-07

LOW MASS GATE: 500.0

MIRROR RATIO: 1.060

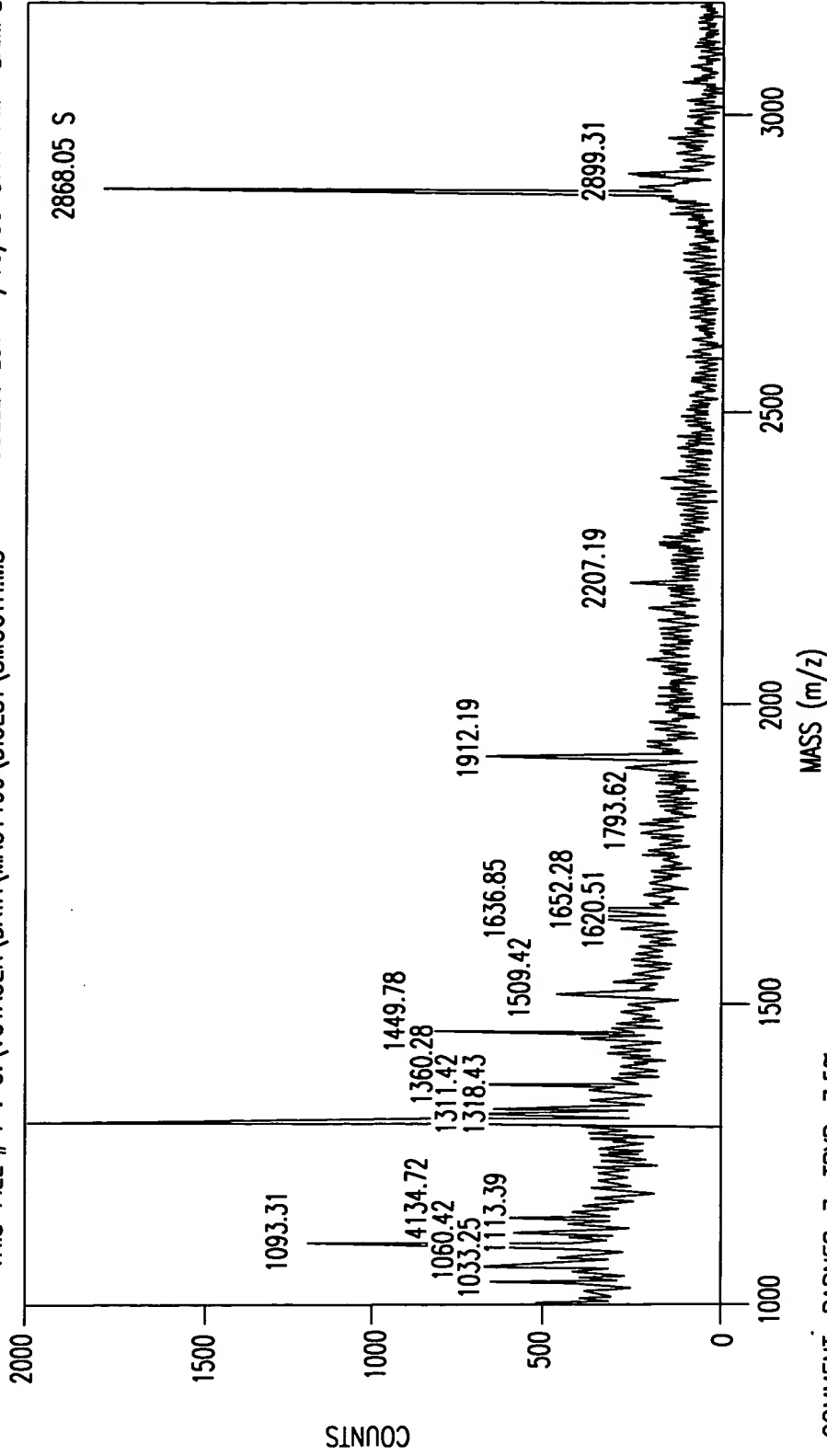
PSD MIRROR RATIO:

TIMED ION SELECTOR: 16.1 OFF

NEGATIVE IONS: OFF

FIG.7F

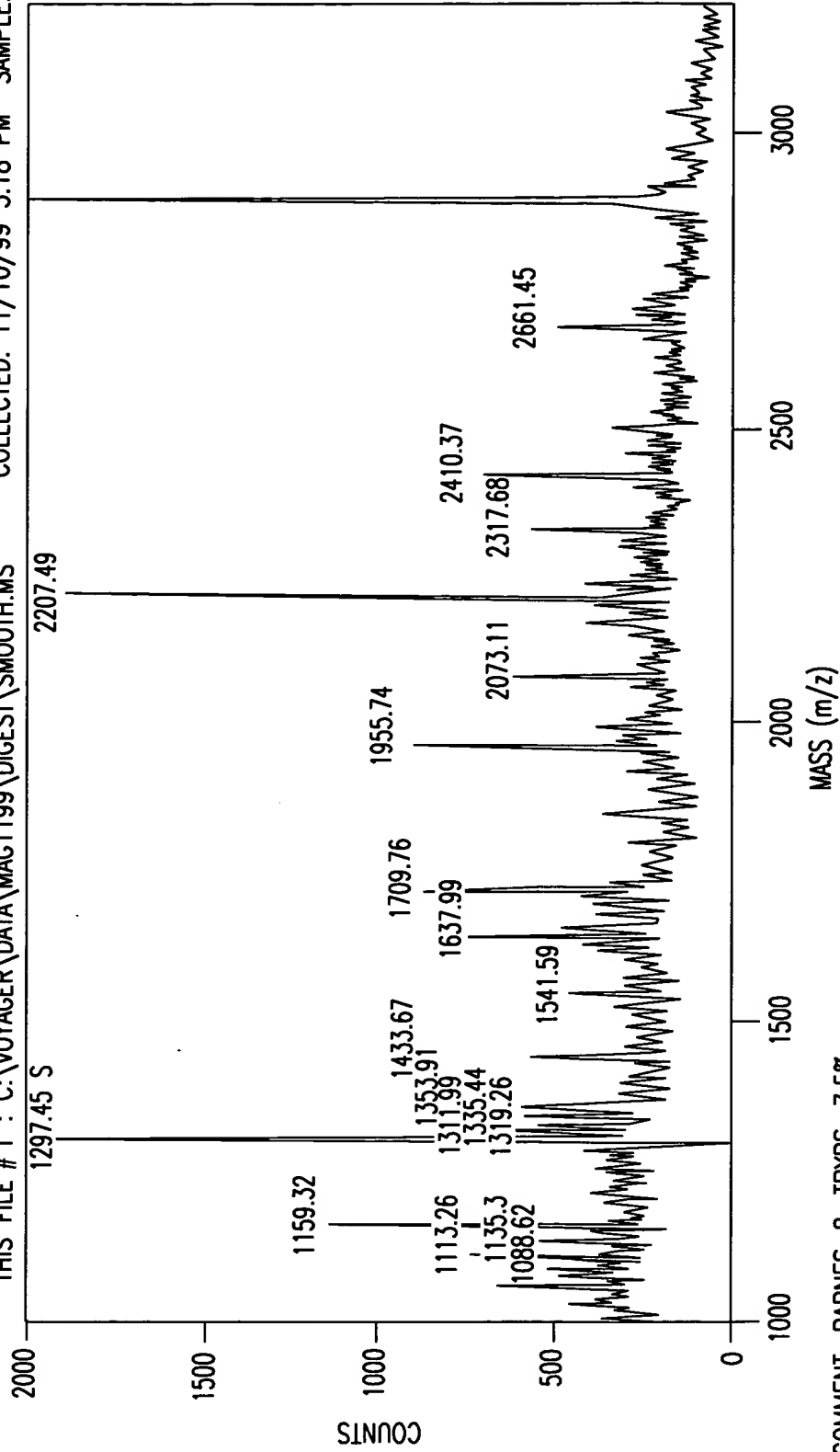
ORIGINAL FILENAME: c:\voyager\data\mag1199\digest\snow_004.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
THIS FILE # 1 : C:\VOYAGER\DATA\MAG1199\DIGEST\SMOOTH.MS COLLECTED: 11/10/99 3:11 PM SAMPLE: 65



COMMENT: BARNES-7, TRYP, 7.5%
METHOD: LDE1000A ACCELERATING VOLTAGE: 20000 LASER: 1965 MIRROR RATIO: 1.060
MODE: LINEAR GRID VOLTAGE: 94.000% SCANS AVERAGED: 256 PSD MIRROR RATIO:
GUIDE WIRE VOLTAGE: 0.075% PRESSURE: 4.06e-07 TIMED ION SELECTOR: 16.1 OFF
DELAY: 50 ON LOW MASS GATE: 500.0 NEGATIVE IONS: OFF

FIG.7G

ORIGINAL FILENAME: c:\voyager\data\mag1199\digest\snow_005.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
THIS FILE # 1 : C:\VOYAGER\DATA\MAG1199\DIGEST\SMOOTH.MS COLLECTED: 11/10/99 3:18 PM SAMPLE: 64



COMMENT: BARNES-8, TRYPS, 7.5%

METHOD: LDE1000A

MODE: LINEAR

ACCELERATING VOLTAGE: 20000

GRID VOLTAGE: 94.000%

GUIDE WIRE VOLTAGE: 0.075%

DELAY: 50 ON

LASER: 1965

SCANS AVERAGED: 256

PRESSURE: 4.01e-07

LOW MASS GATE: 500.0

MIRROR RATIO: 1.060

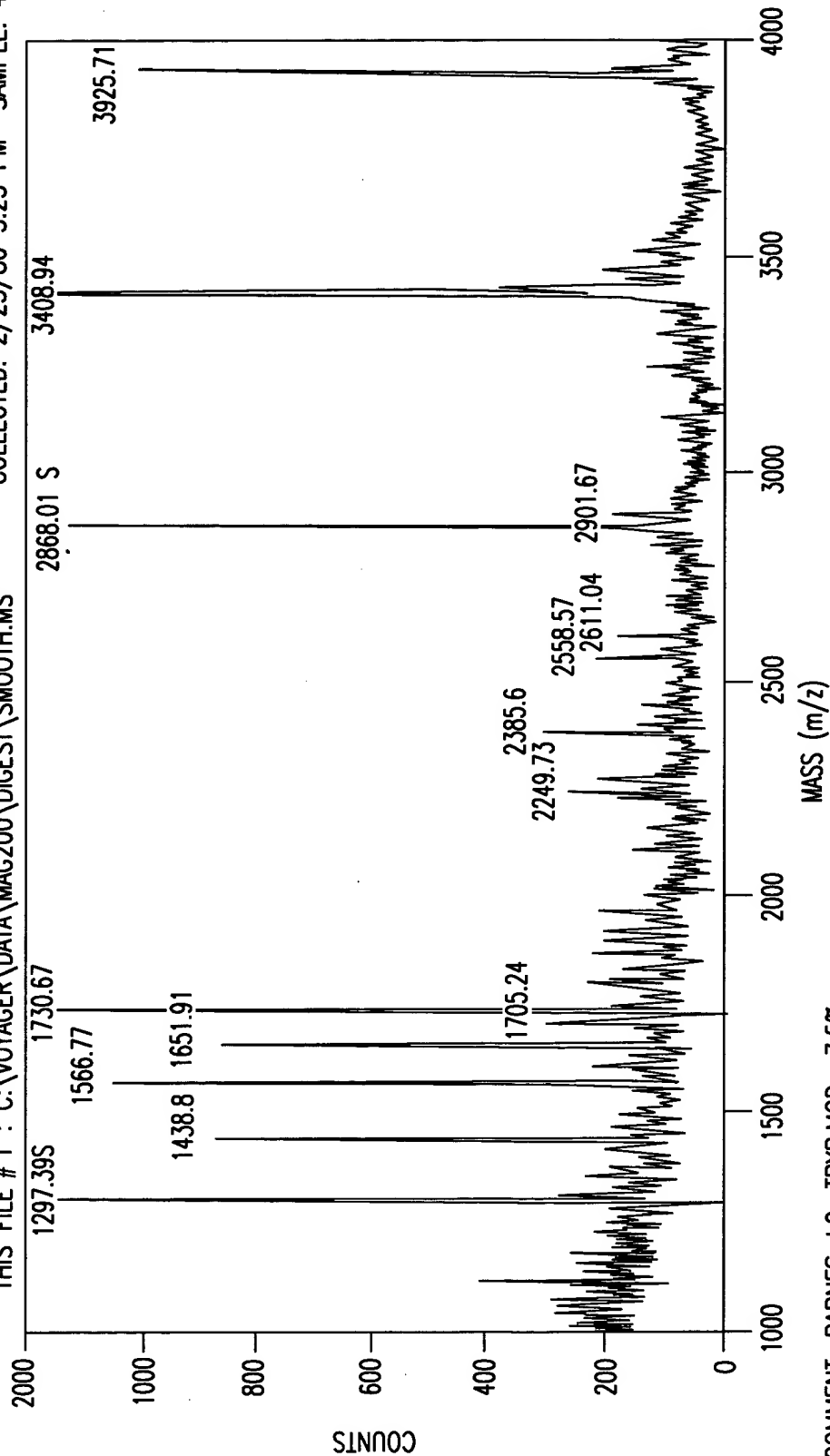
PSD MIRROR RATIO:

TIMED ION SELECTOR: 16.1 OFF

NEGATIVE IONS: OFF

FIG.7H

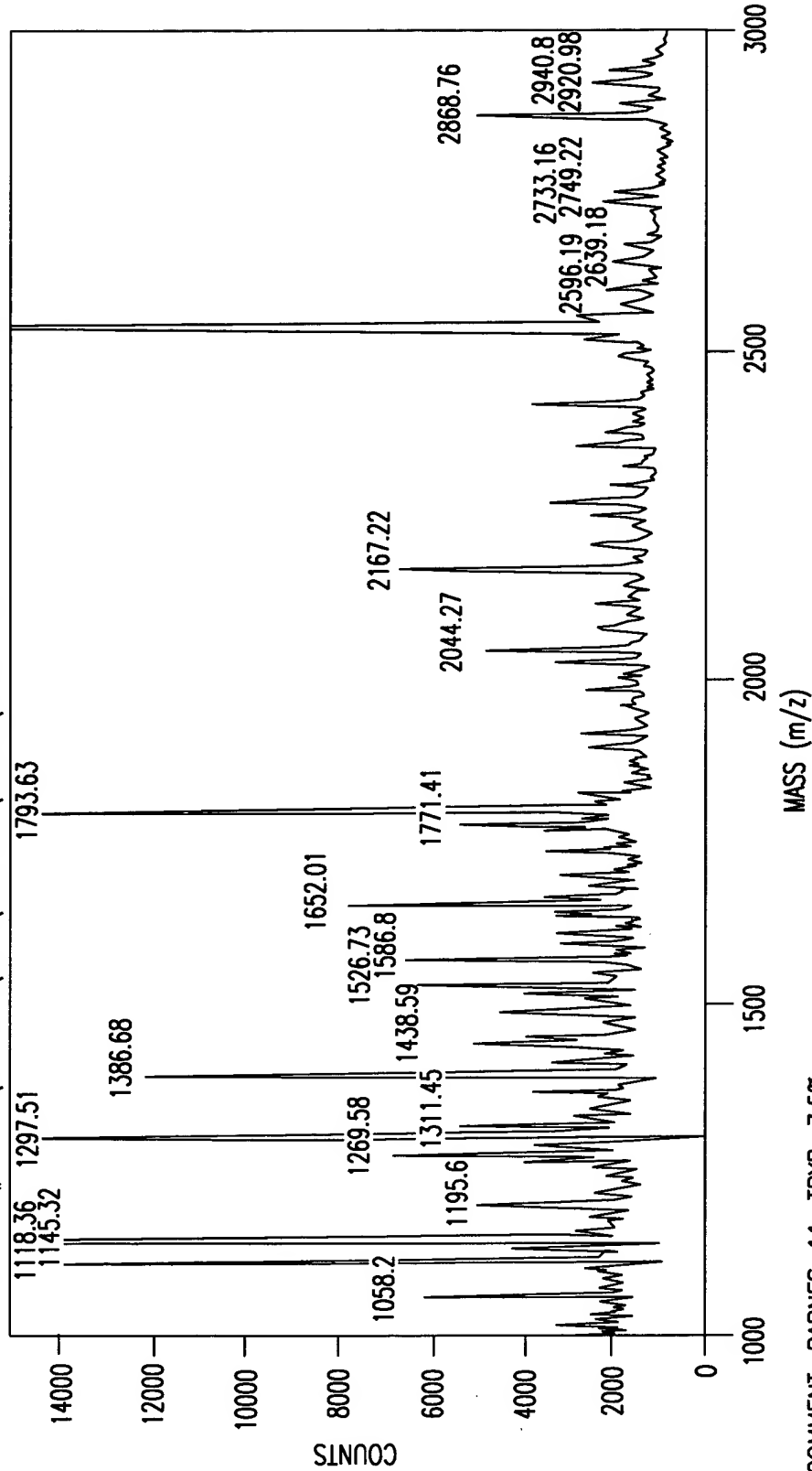
ORIGINAL FILENAME: c:\voyager\data\mag200\digest\barne007.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
 THIS FILE # 1 : C:\VOYAGER\DATA\MAG200\DIGEST\SMOOTH.MS COLLECTED: 2/23/80 3:25 PM SAMPLE: 44



COMMENT: BARNES-b9, TRYP.MOD., 7.5%
 METHOD: LDE1000A ACCELERATING VOLTAGE: 25000 LASER: 1860 MIRROR RATIO: 1.080
 MODE: LINEAR GRID VOLTAGE: 94.000% SCANS AVERAGED: 256 PSD MIRROR RATIO:
 GUIDE WIRE VOLTAGE: 0.090% PRESSURE: 3.27e-07 TIMED ION SELECTOR: 16.1 OFF
 DELAY: 50 ON LOW MASS GATE: 500.0 NEGATIVE IONS: OFF

FIG.71

ORIGINAL FILENAME: c:\voyager\data\mag1299\digest\barne004.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
THIS FILE # 2 : C:\VOYAGER\DATA\MAG1299\DIGEST\SMOOTH.MS COLLECTED: 12/15/99 3:49 PM SAMPLE: 14



COMMENT: BARNES-11, TRYP, 7.5%

METHOD: LDE1000A

MODE: LINEAR

ACCELERATING VOLTAGE: 25000

GRID VOLTAGE: 94.000%

GUIDE WIRE VOLTAGE: 0.090%

DELAY: 50 ON

LASER: 1965

SCANS AVERAGED: 256

PRESSURE: 5.84e-07

LOW MASS GATE: 500.0

MIRROR RATIO: 1.080

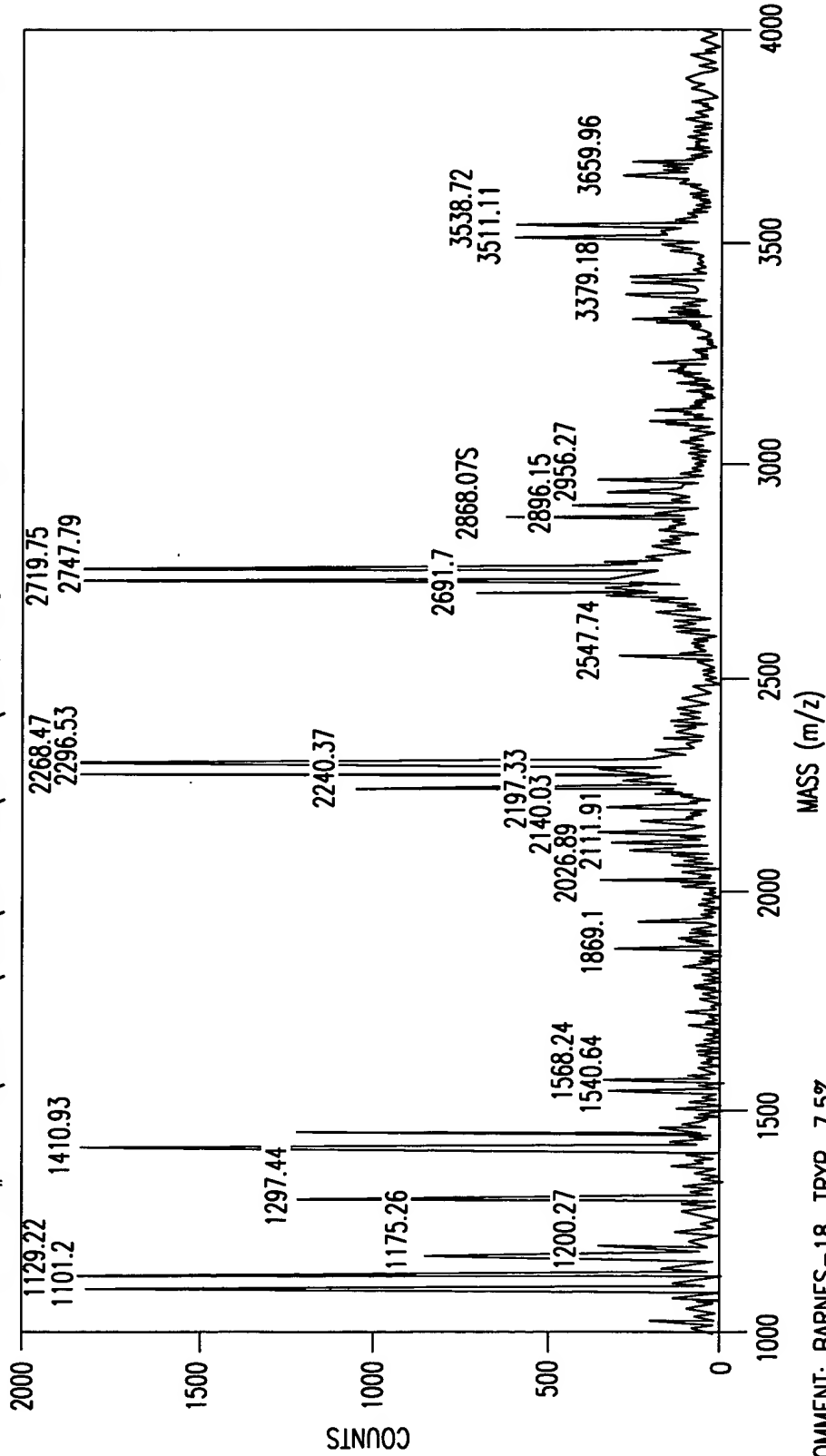
PSD MIRROR RATIO:

TIMED ION SELECTOR: 16.1 OFF

NEGATIVE IONS: OFF

FIG.7J

ORIGINAL FILENAME: c:\voyager\data\mag1299\digest\barne005.ms
 THIS FILE # 2 : C:\VOYAGER\DATA\MAG1299\DIGEST\SMOOTH.MS
 SAVITSKY-GOLAY ORDER=2 POINTS=19
 COLLECTED: 12/15/99 4:47 PM SAMPLE: 13



COMMENT: BARNES-18, TRYP, 7.5%

METHOD: LDE1000A
 MODE: LINEAR

ACCELERATING VOLTAGE: 25000

GRID VOLTAGE: 94.000%

GUIDE WIRE VOLTAGE: 0.090%

DELAY: 50 ON

LASER: 1745

SCANS AVERAGED: 256

PRESSURE: 2.90e-07

LOW MASS GATE: 500.0

MIRROR RATIO: 1.080

PSD MIRROR RATIO:

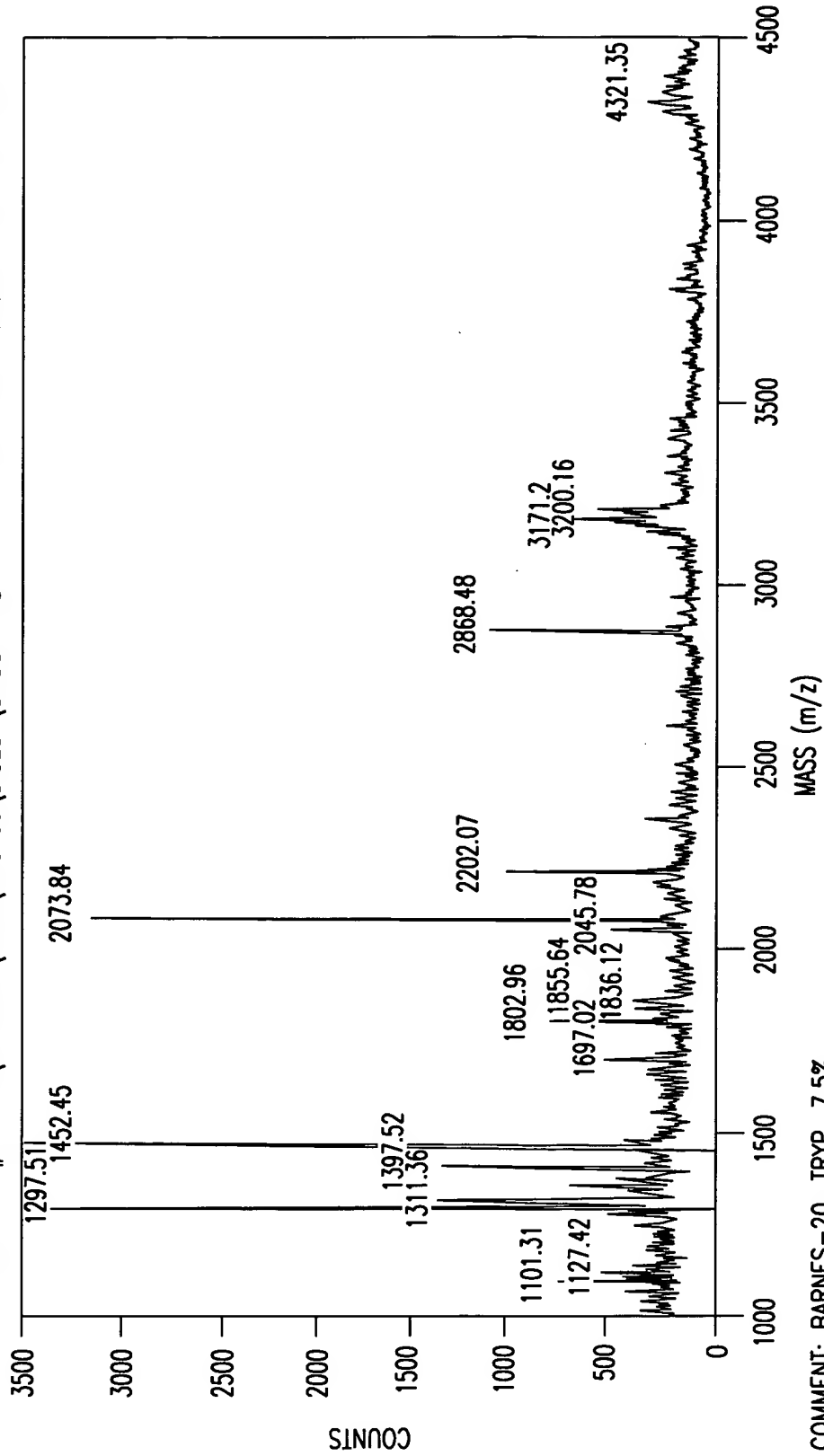
TIMED ION SELECTOR: 16.1 OFF

NEGATIVE IONS: OFF

FIG. 7K

SAVITSKY-GOLAY ORDER=2 POINTS=19
COLLECTED: 1/6/80 3:36 PM SAMPLE: 42

ORIGINAL FILENAME: c:\voyager\data\mag100\digest\borne001.ms
THIS FILE # 2 : C:\VOYAGER\DATA\MAG100\DIGEST\SMOOTH.MS



COMMENT: BARNES-20, TRYP, 7.5%

METHOD: LDE1000A
MODE: LINEAR

ACCELERATING VOLTAGE: 25000

GRID VOLTAGE: 94.000%

GUIDE WIRE VOLTAGE: 0.090%

DELAY: 50 ON

LASER: 1820

SCANS AVERAGED: 256

PRESSURE: 9.21e-07

LOW MASS GATE: 500.0

MIRROR RATIO: 1.080

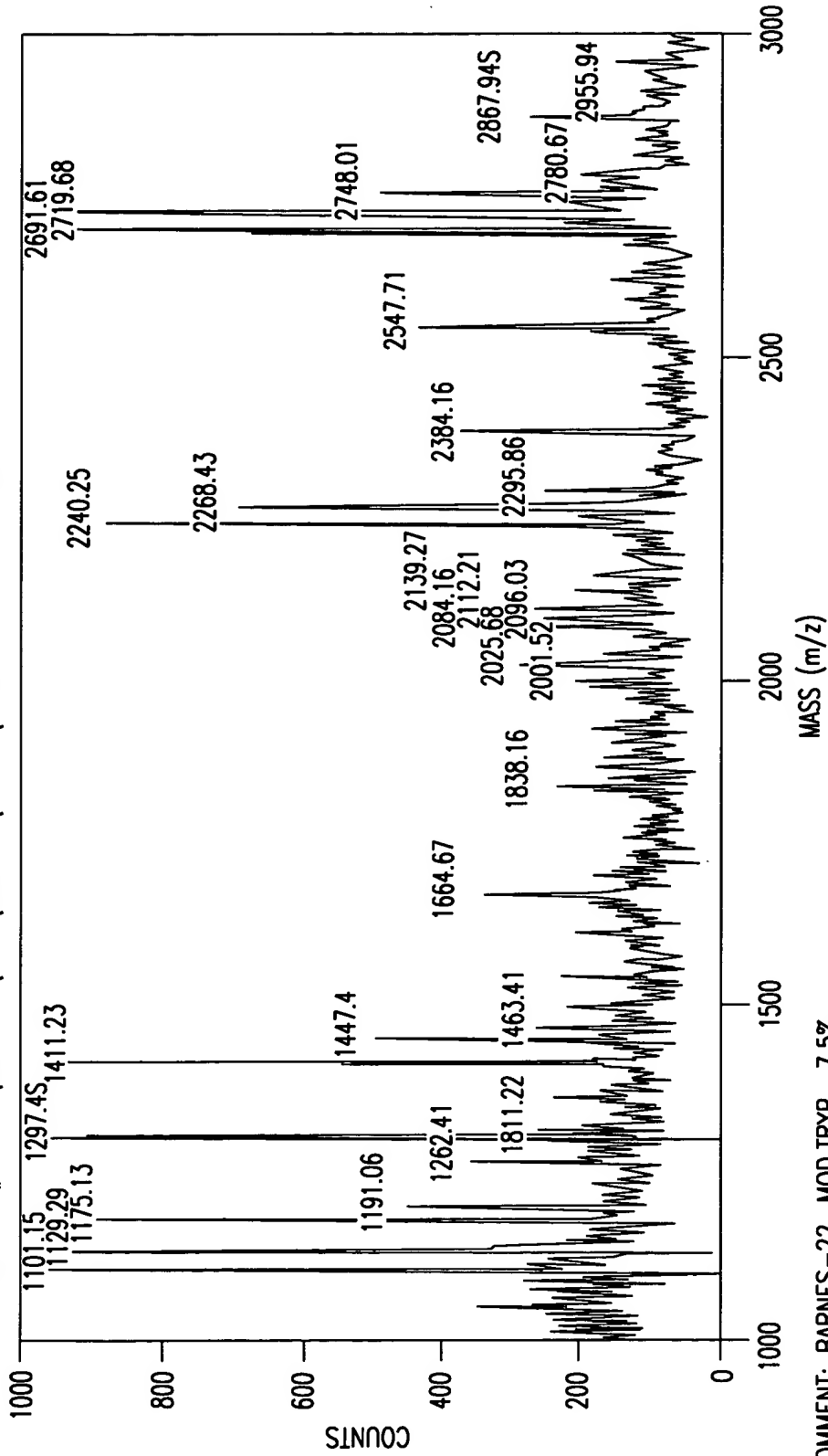
PSD MIRROR RATIO:

TIMED ION SELECTOR: 16.1 OFF

NEGATIVE IONS: OFF

FIG.7L

ORIGINAL FILENAME: c:\voyager\data\mag200\digest\barne003.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
THIS FILE # 1 : C:\VOYAGER\DATA\MAG200\DIGEST\SMOOTH.MS COLLECTED: 2/16/80 3:35 PM SAMPLE: 54



COMMENT: BARNES-22, MOD.TRYP., 7.5%

METHOD: LDE1000A

MODE: LINEAR

ACCELERATING VOLTAGE: 25000

GRID VOLTAGE: 94.000%

GUIDE WIRE VOLTAGE: 0.090%

DELAY: 50 ON

LASER: 1870

SCANS AVERAGED: 231

PRESSURE: 3.43e-07

LOW MASS GATE: 500.0

MIRROR RATIO: 1.080

PSD MIRROR RATIO:

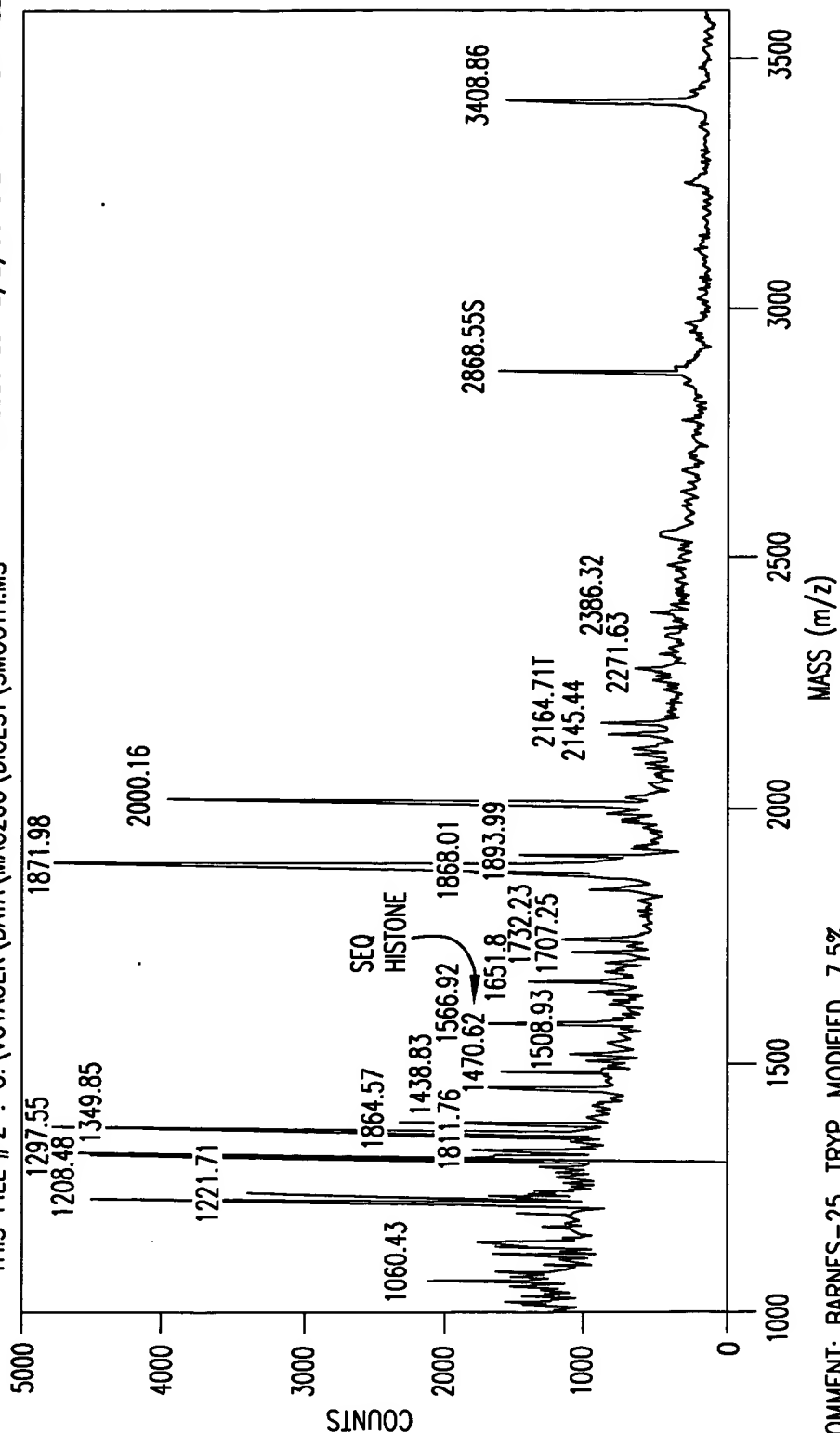
TIMED ION SELECTOR: 16.1 OFF

NEGATIVE IONS: OFF

FIG. 7M

SAVITSKY-GOLAY ORDER=2 POINTS=19
COLLECTED: 2/2/80 3:24 PM SAMPLE: 62

ORIGINAL FILENAME: c:\voyager\data\mag200\digest\barne001.ms
THIS FILE # 2 : C:\VOYAGER\DATA\MAG200\DIGEST\SMOOTH.MS



COMMENT: BARNES-25, TRYP. MODIFIED, 7.5%

METHOD: LDE1000A
MODE: LINEAR

ACCELERATING VOLTAGE: 25000
GRID VOLTAGE: 94.000%
GUIDE WIRE VOLTAGE: 0.090%

LASER: 1860

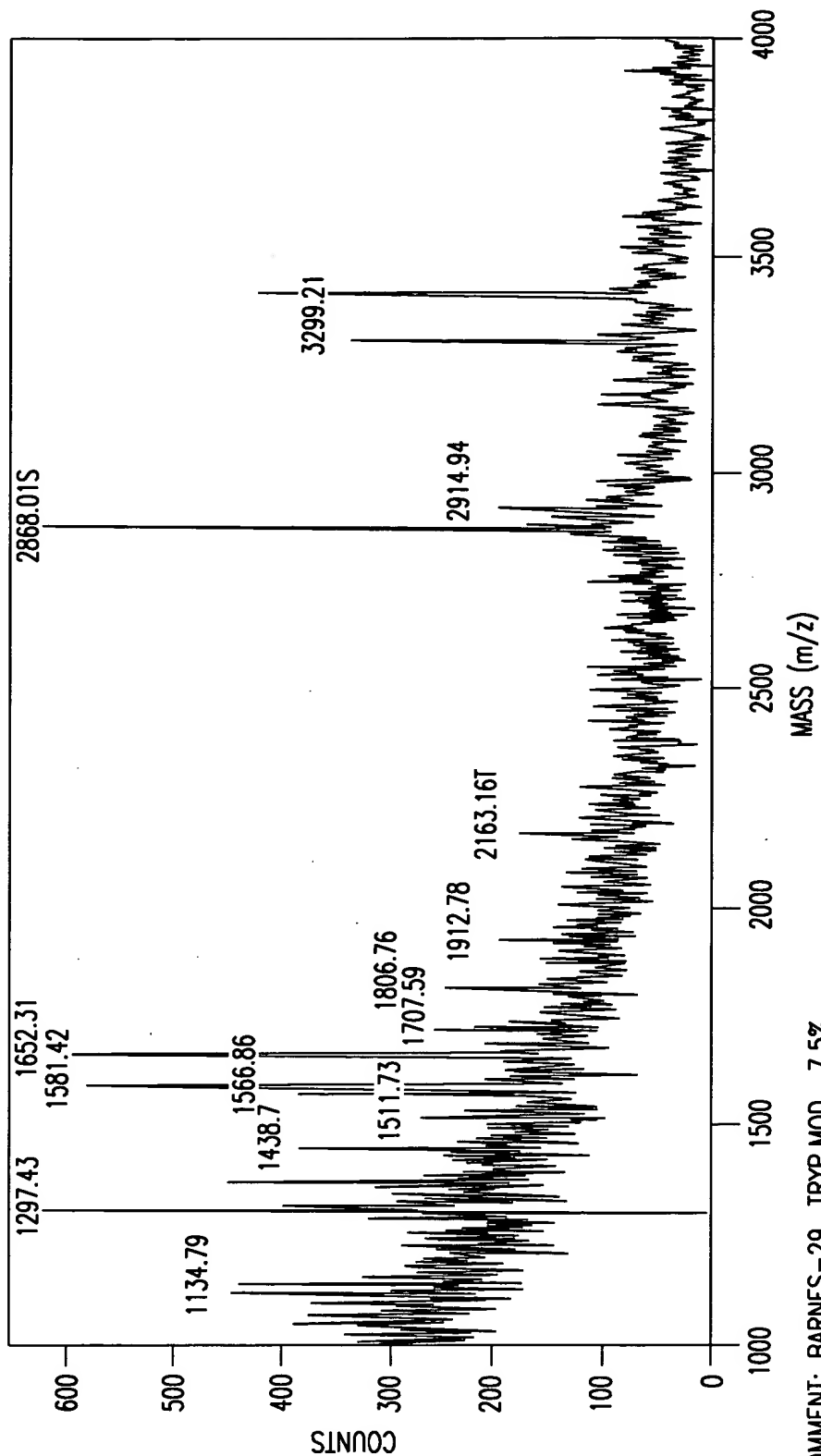
SCANS AVERAGED: 256
PRESSURE: 9.26e-07
LOW MASS GATE: 500.0

MIRROR RATIO: 1.080

PSD MIRROR RATIO:
TIMED ION SELECTOR: 16.1 OFF
NEGATIVE IONS: OFF

FIG.7N

ORIGINAL FILENAME: c:\voyager\data\mag200\digest\barne006.ms SAVITSKY-GOLAY ORDER=2 POINTS=19
THIS FILE # 2 : C:\VOYAGER\DATA\MAG200\DIGEST\SMOOTH.MS COLLECTED: 2/23/80 3:19 PM SAMPLE: 43



COMMENT: BARNES-29, TRYP.MOD., 7.5%

METHOD: LDE1000A
MODE: LINEAR

ACCELERATING VOLTAGE: 25000
GRID VOLTAGE: 94.000%
GUIDE WIRE VOLTAGE: 0.090%
DELAY: 50 ON

LASER: 1860
SCANS AVERAGED: 256
PRESSURE: 3.82e-07
LOW MASS GATE: 500.0

MIRROR RATIO: 1.080
PSD MIRROR RATIO:
TIMED ION SELECTOR: 16.1 OFF
NEGATIVE IONS: OFF

FIG.70



FIG.8

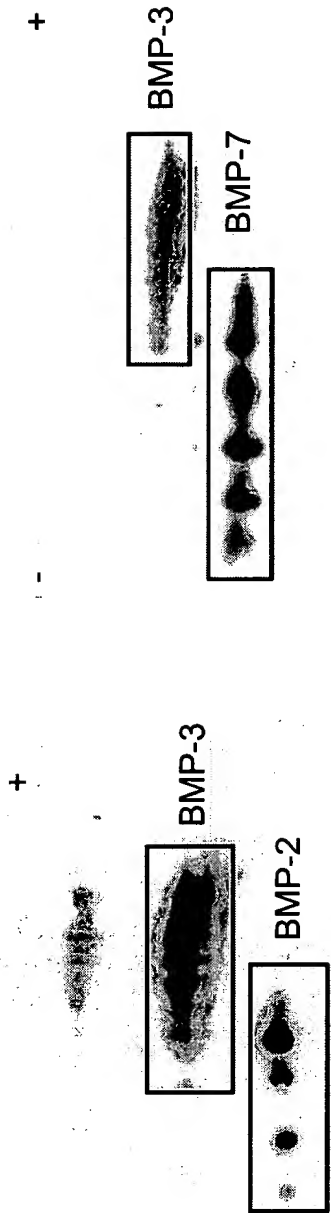


FIG. 9B

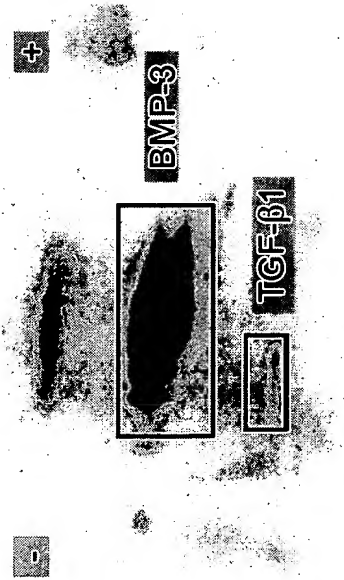


FIG. 9D

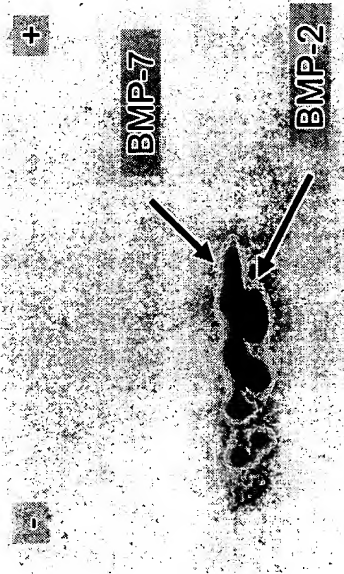


FIG. 9C

FIG. 9A

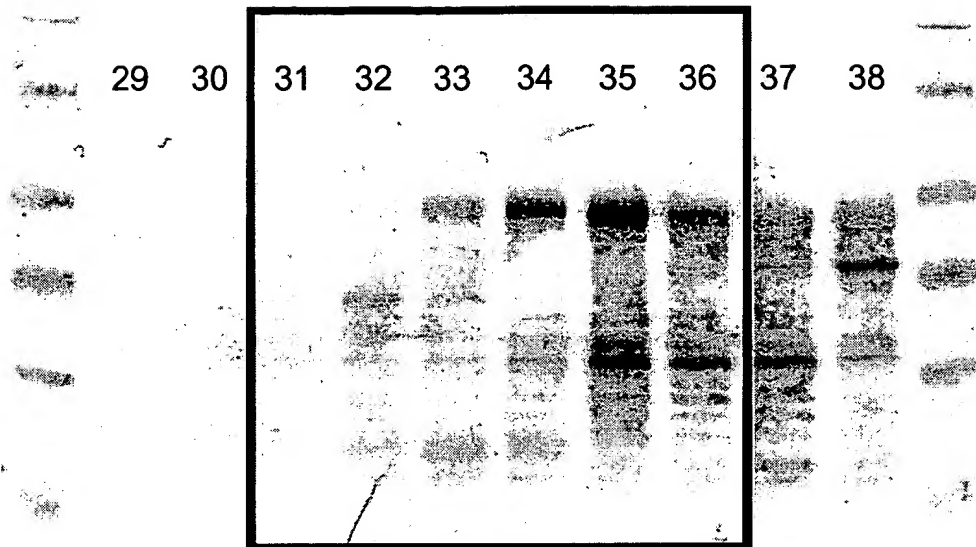


FIG.10

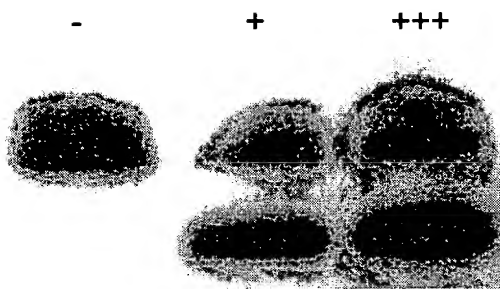


FIG.11

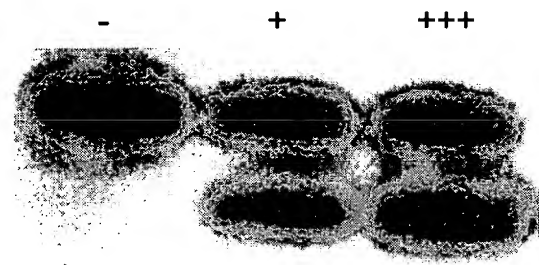


FIG.12

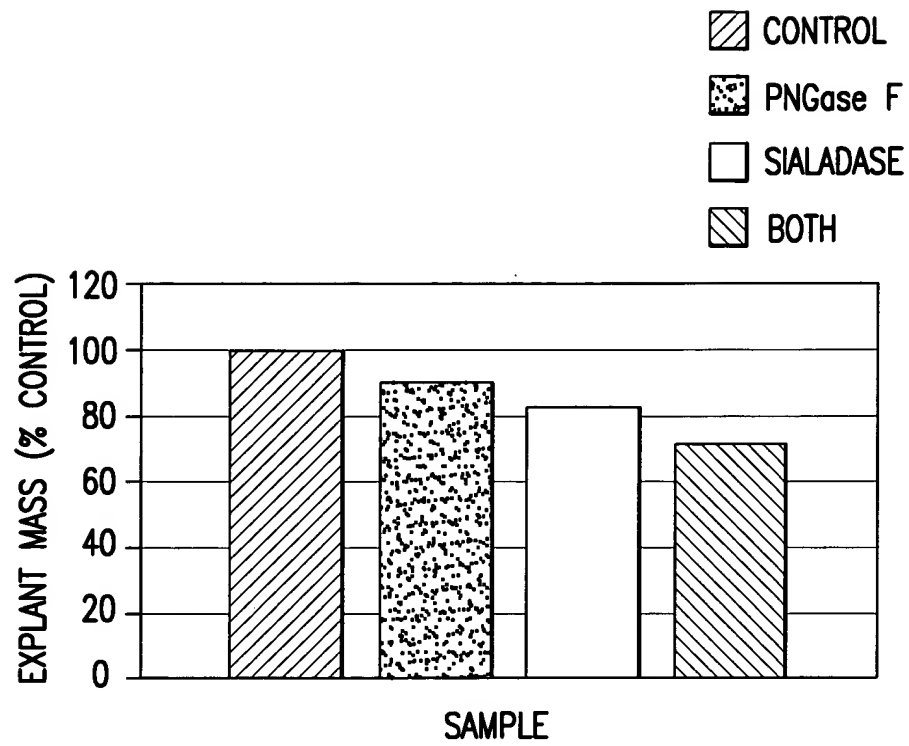


FIG. 13A

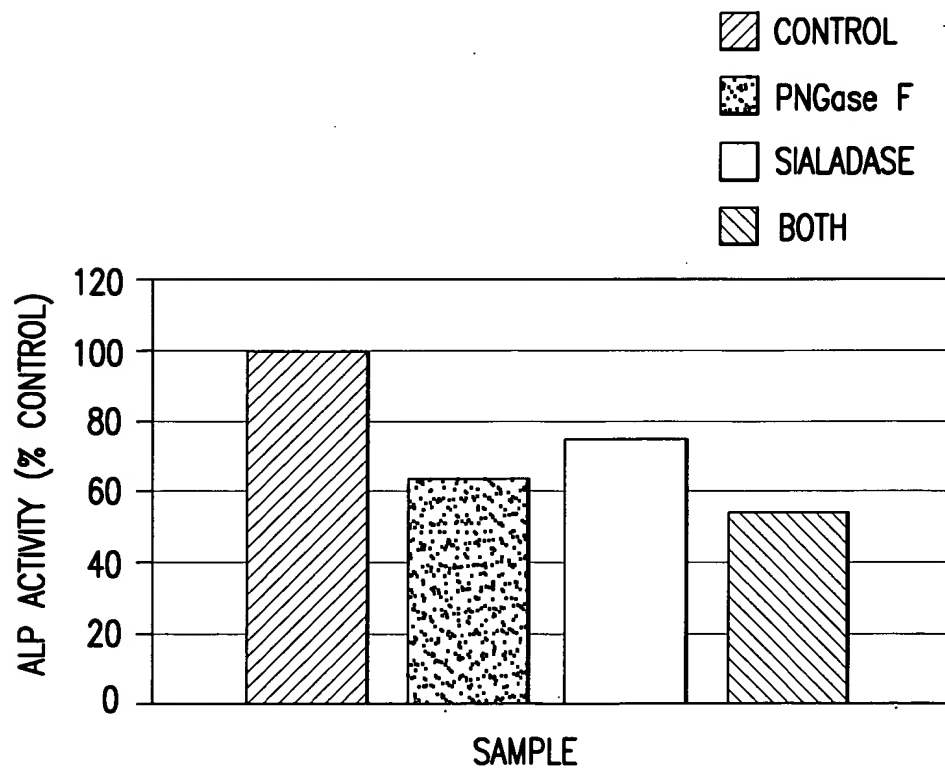


FIG. 13B

ANTIBODY LISTING

SPECIFICITY	ANTIGEN	HOST SPECIES	PC/MC	SOURCE	CATALOG NO.
TGF- β 1(HUMAN)	PROTEIN	RABBIT	POLYCLONAL	PROMEGA	G1221
TGF- β 2(HUMAN)	PEPTIDE	RABBIT	POLYCLONAL	SANTA CRUZ BIOTECHNOLOGY	sc-90
TGF- β 3(HUMAN)	PEPTIDE	RABBIT	POLYCLONAL	SANTA CRUZ BIOTECHNOLOGY	sc-82
BMP-2 (HUMAN)	PROTEIN	RABBIT	POLYCLONAL	AUSTRAL BIOLOGICS	PA-513-9
BMP-3 (HUMAN)	PEPTIDE	CHICKEN	POLYCLONAL	RESEARCH GENETICS	NA
BMP-4 (HUMAN)	PEPTIDE	GOAT	POLYCLONAL	SANTA CRUZ BIOTECHNOLOGY	so-6896
BMP-5 (HUMAN)	PEPTIDE	GOAT	POLYCLONAL	SANTA CRUZ BIOTECHNOLOGY	sc-7405
BMP-6 (HUMAN)	PEPTIDE	MOUSE	MONOCLONAL	NOVOCASTRA LABORATORIES	NCL-BMP6
BMP-7 (HUMAN)	PEPTIDE	RABBIT	POLYCLONAL	RESEARCH GENETICS	NA
FGF-1 (HUMAN)	PEPTIDE	GOAT	POLYCLONAL	SANTA CRUZ BIOTECHNOLOGY	sc-1884
OSTEONECTIN (BOVINE)	PROTEIN	MOUSE	MONOCLONAL	DSHB	AON-1
OSTEONECTIN (BOVINE)	PROTEIN	RABBIT	POLYCLONAL	ACCURATE CHEMICALS	A761/R1H
SERUM ALBUMIN (BOVINE)	PROTEIN	RABBIT	POLYCLONAL	CHEMICON INTERNATIONAL	AB870
TRANSFERRIN (HUMAN)	PROTEIN	CHICKEN	POLYCLONAL	CHEMICON INTERNATIONAL	AB797
apo-A1 LIPOPROTEIN (HUMAN)	PROTEIN	GOAT	POLYCLONAL	CHEMICON INTERNATIONAL	AB740

FIG.14

IDENTIFICATION OF PROTEINS BY AMINO ACID SEQUENCING OF TRYPTIC FRAGMENTS FROM ID GELS

BAND	SAMPLE	SEQUENCE DATA	BEST DATABASE MATCH	MATCH	IDENTIFICATION	SPECIES	ACC. NO.	AAs	SEQ ID NO:
1									
2	fx 49 (1579)	XLAAAGYDVEK	ALAAAGYDVEK	11/11	HISTONE H1.c	HUMAN	87668 (NCBI)	65-75	1
3	fx 67 (1346)	SLEKVCADLIR	SLEKVCADLIR	11/11	40s RIBOSOMAL PROTEIN S20	RAT	R3RT20 (PIR)	31-41	2
4	fx 55 0	(V)VCGMLGFPSEAPV	VVCGMLGFPGEKRV	11/14	LORP	MOUSE	AAC95338 (NCBI)	213- 226	3
5	N TERMINAL seq	STGVLLPLQNNELPG	STGVLLPLQNNELPG	15/15	BMP-3	HUMAN	4557371 (NCBI)	290- 304	4
	fx 72 (3925)	STGVLLPLQNNELPGA EYQY	STGVLLPLQNNELPGA AEYQY	20/20	BMP-3	HUMAN	4557371 (NCBI)	290- 304	5
	fx 74 (3409)	STGVLLPLQ	STGVLLPLQ	9/9	BMP-3	HUMAN	4557371 (NCBI)	290- 298	6
6	fx 55 (1566)	(S)QTLQFXE	SQTLQFDE	7/8	BMP-3	HUMAN	4557371 (NCBI)	346- 353	7
	fx 47	VYAF	NO MATCH		???				8
	N TERMINAL SEQ	HAGKYSREKNT(P)A(P)	HGGKYSREKNQPKP	11/14	α 2-MACROGLOBULIN RECEPTOR ASSOC. PRO.	HUMAN	P30533 (SWISS-PROT)	31-46	9
	fx 57 (1438)	SQTLQFDEQ	SQTLQFDEQ	9/9	BMP-3	HUMAN	4557371 (NCBI)	346- 354	10
	fx 57 (1652)	SLKPSNHA	SLKPSNHA	8/8	BMP-3	HUMAN	4557371 (NCBI)	410- 417	11
7	fx 51 (1093)	AALRPLVKP	AALRPLVKP	9/9	60s RIBOSOMAL PROTEIN L32	MOUSE	P17932 (SWISS-PROT)	1-9	
	fx 37 (NO MS)	A(H)I(Q)VERYV	AIVER	5/5	60s RIBOSOMAL PROTEIN L32	MOUSE	P17932 (SWISS-PROT)	109- 113	12
	fx 37 (NO MS)	A(H)I(Q)VERYV	HQSDRYV	5/7	60s RIBOSOMAL PROTEIN L32	MOUSE	P17932 (SWISS-PROT)	22-28	12
8	fx 78 ()	XALF(G)AQLGXALGPI	NO MATCH		???				13
9	fx 56 (1567)	SQTLQFDEQT	SQTLQFDEQT	10/10	BMP-3	HUMAN	P12645 (SWISS-PROT)	346- 355	14

FIG.15A

IDENTIFICATION OF PROTEINS BY AMINO ACID SEQUENCING OF TRYPTIC FRAGMENTS FROM ID GELS

BAND	SAMPLE	SEQUENCE DATA	BEST DATABASE MATCH	MATCH	IDENTIFICATION	SPECIES	ACC. NO.	AAs	SEQ ID NO:
11	fx 55 (1311)	SQTLXF	SQTLQF	5/6	BMP-3	HUMAN	4557371 (NCBI)	346- 351	15
	fx 47 (1772)	VLATVTKPVGGDK	VLATVTKPVGGDK	13/13	60s RIBOSOMAL PROTEIN L6	HUMAN	Q02878 (SWISS-PROT)	87-99	16
	fx 76 (1795)	xVFAL	VFAL	4/4	60s RIBOSOMAL PROTEIN L6	HUMAN	Q02878 (SWISS-PROT)	273- 276	17
	fx 61 (1145)	AVPQLQGYLR	AIPQLQGYLR	9/10	60s RIBOSOMAL PROTEIN L6	HUMAN	Q02878 (SWISS-PROT)	262- 271	18
18									
22	fx 69 (1145)	ALDAAYCFR	ALDAAYCFR	9/9	TGF- β 2	HUMAN	P08112 (SWISS-PROT)	303- 311	19
	fx 58 (NO MATCH)	GYNANFCAGACPYL	GYNANFCAGACPYL	14/14	TGF- β 2	HUMAN	P08112 (SWISS-PROT)	340- 353	20
	fx 66 (1411.71)	VNSQSLSPY	VNSQSLSPY	9/9	SPP24	BOVINE	Q27967 (SWISS-PROT)	42-50	21
25	fx 39 (1470)	KAAPSPV(P)	KAAPSPVP	8/8	HISTONE H1.x	HUMAN	JC4928 (PIR)	199- 206	22
29									

fx = FRACTION NUMBER (MOLECULAR WEIGHT OF FRAGMENT, AS MEASURED BY SDS-PAGE)

FIG.15B

IDENTIFICATION OF PROTEINS BY MASS SPECTROMETRY OF TRYPTIC FRAGMENTS FROM 1D GELS

BAND	MASS SPEC PROFILE	SPECIES	ACC. NO.	MASS SPEC DATA	MASS SPEC DATABASE	MASS DIFFERENCE	AAs	% COVERAGE	COMMENTS
1	4 PEAKS MATCH WITH HISTONE H1.c	HUMAN	87668 (NCBI)	1172.97	1172.37	0.60	110-121	22	15 MS PEAKS MATCH WITH BAND 2
				1579.87	1579.71	0.16	65-79		
				1708.47	1707.89	0.58	64-79		
				2011.58	2012.32	-0.74	35-54		
2	3 PEAKS MATCH WITH HISTONE H1.c	HUMAN	87668 (NCBI)	1579.76	1579.71	0.05	65-79*	16	IDENTIFICATION OF STARRED PEPTIDE CONFIRMED BY SEQUENCE ANALYSIS
				1708.02	1707.89	0.13	64-79		
				2012.12	2012.32	-0.20	35-54		
3	7 PEAKS MATCH WITH RIBOSOME S20	RAT	R3RT20 PIR	1129.76	1129.40	0.36	50-59	62	15 MS PEAKS MATCH WITH BAND 1
				1156.21	1156.30	-0.09	76-83		
				1334.46	1334.62	-0.16	56-66		
				1352.13	1351.58	0.55	88-99		
				1518.04	1517.77	0.27	9-21		
				1919.02	1919.19	-0.17	5-21		
				3404.02	3404.87	-0.85	88-119		
4	3 PEAKS MATCH WITH LYSYL OXIDASE RP	HUMAN	NP002309 (SWISS-PROT)	1987.95	1988.27	-0.32	150-167	8	12 MS PEAKS MATCH WITH BAND 8
				2410.35	2410.63	-0.28	648-669		
				2610.57	2610.10	0.47	455-478		

FIG.16A

IDENTIFICATION OF PROTEINS BY MASS SPECTROMETRY OF TRYPTIC FRAGMENTS

BAND	MASS SPEC PROFILE	SPECIES	ACC. NO.	MASS SPEC DATA	MASS SPEC DATABASE	MASS DIFFERENCE	AAS	% COVERAGE	COMMENTS
5	9 PEAKS MATCH WITH BMP-3	HUMAN	4557371 (NCBI)	1113.32	1113.31	0.01	361-368	48	% COVERAGE CALCULATION IS RELATIVE TO THE MATURE BMP-3, 183 AAS (290-472)
				1438.53	1438.58	-0.05	346-357		
				1566.76	1566.76	0.00	345-357		
				1651.86	1651.91	-0.05	410-424		
				1794.09	1794.02	0.07	346-360		
				2268.46	2268.63	-0.17	374-392		
				2424.45	2424.81	-0.36	373-392		
6	3 PEAKS MATCH WITH α 2- MACROGLOBULIN RAP	HUMAN	P30533 (SWISS-PROT)	3409.15	3407.77	1.38	290-318*	17	IDENTIFICATION OF STARRED PEPTIDE CONFIRMED BY SEQUENCE ANALYSIS
				1002.24	1002.15	0.09	283-290		
				2362.58	2362.43	0.15	129-150		
				3048.51	3048.52	-0.01	257-282		
				1566.93	1566.75	0.18	346-357		
	2 PEAKS MATCH WITH BMPS-3	HUMAN	4557371 (NCBI)	1651.88	1651.91	-0.03	410-424	15	% COVERAGE CALCULATION IS RELATIVE TO THE MATURE BMP-3, 183 AAS (290-472)

FIG. 16B

IDENTIFICATION OF PROTEINS BY MASS SPECTROMETRY OF TRYPTIC FRAGMENTS FROM 1D GELS

BAND	MASS SPEC PROFILE	SPECIES	ACC. NO.	MASS SPEC DATA	MASS SPEC DATABASE	MASS DIFFERENCE	AAS	% COVERAGE	COMMENTS
7	4 PEAKS MATCH WITH RIBOSOME L32	MOUSE	P17932 (SWISS-PROT)	1033.25	1033.17	0.08	67-75	33	
				1093.31	1093.40	-0.09	1-10*		
				1134.72	1134.28	0.44	65-74		
				1449.78	1449.66	0.12	19-29		
				1060.42	1060.20	0.22	102-111	21	% COVERAGE CALCULATION IS RELATIVE TO THE MATURE BMP-3, 183 AAS (290-472)
8	1 PEAK MATCHES WITH LYSYL OXIDASE RP	HUMAN	NP002309 (SWISS-PROT)	1113.39	1113.31	0.08	361-368		
				1360.26	1360.58	-0.32	190-200		
				1652.28	1651.91	0.37	410-424		
				1793.62	1794.02	-0.40	346-360		
				2410.37	2410.63	-0.26	648-669	3	12 MS PEAKS MATCH WITH BAND 4
9	6 PEAKS MATCH WITH BMP-3	HUMAN	4557371 (NCBI)	1113.14	1113.31	-0.17	361-368	36	% COVERAGE CALCULATION IS RELATIVE TO THE MATURE BMP-3, 183 AAS (290-472)
				1438.60	1438.58	0.02	346-357		
				1566.77	1566.76	0.01	345-357		
				1651.91	1651.61	0.30	410-424		
				2901.67	2901.19	0.48	41-66		
				3408.94	3407.77	1.17	290-318		

FIG.16C

IDENTIFICATION OF PROTEINS BY MASS SPECTROMETRY OF TRYPTIC FRAGMENTS FROM 1D GELS

BAND	MASS SPEC PROFILE	SPECIES	ACC. NO.	MASS SPEC DATA	MASS SPEC DATABASE	MASS DIFFERENCE	AAS	% COVERAGE	COMMENTS
11	5 PEAKS MATCH WITH BMP-3	MOUSE	4557371 (NCBI)	1113.23	1113.31	-0.08	361-368	48	% COVERAGE CALCULATION IS RELATIVE TO THE MATURE BMP-3, 183 AAS (290-472)
				1651.73	1651.91	-0.18	410-424		
				1793.58	1794.02	-0.44	346-360		
				2424.24	2424.81	-0.57	373-392		
				3408.34	3407.77	0.57	290-318		
18	5 PEAKS MATCH WITH RIBOSOME L6	HUMAN	Q02878 (SWISS-PROT)	1140.38	1140.23	0.15	114-122	16	
				1526.88	1526.86	0.02	141-155		
		MOUSE	P47911 (SWISS-PROT)	1059.15	1059.12	0.03	10-20		
				1145.36	1145.35	0.01	262-271		
				1386.74	1386.68	0.06	260-271		
	4 PEAKS MATCH WITH TGF- β 2	HUMAN	P08112 (SWISS-PROT)	1101.20	1101.26	-0.06	303-311	52	
				1175.26	1175.42	-0.16	400-409		
				2240.37	2240.60	-0.23	312-328		
				2691.70	2691.91	-0.21	340-362		
	5 PEAKS MATCH WITH SPP24	BOVINE	Q27967 (SWISS-PROT)	1410.93	1411.60	-0.67	42-53	30	
				1447.59	1477.65	-0.06	113-124		
				1540.64	1540.60	0.04	86-98		
				1869.10	1869.05	0.05	62-77		
				2268.47	2268.57	-0.10	33-53		

FIG.16D

IDENTIFICATION OF PROTEINS BY MASS SPECTROMETRY OF TRYPTIC FRAGMENTS FROM 1D GELS

BAND	MASS SPEC PROFILE	SPECIES	ACC. NO.	MASS SPEC DATA	MASS SPEC DATABASE	MASS DIFFERENCE	AAS	% COVERAGE	COMMENTS
22	5 PEAKS MATCH WITH TGF- β 2	HUMAN	P08112 (SWISS-PROT)	1101.15	1101.26	-0.11	303-311	48	
				1175.13	1175.42	-0.29	400-409		
				2084.16	2084.42	-0.26	312-347		
				2240.25	2240.60	-0.35	312-328		
				2691.61	2891.91	-0.30	340-362		
25	2 PEAKS MATCH WITH SPP24	BOVINE	Q27967 (SWISS-PROT)	1411.23	1411.60	-0.37	42-53	11	
				1447.40	1447.65	-0.25	113-124		
				1208.46	1208.40	0.06	48-57		
	5 PEAKS MATCH WITH HISTONE H1.x	HUMAN	JC4928 (SWISS-PROT)	1221.71	1222.35	-0.64	107-118	14	
				1349.85	1350.52	-0.67	107-119		
				1364.57	1364.59	-0.02	48-58		
				1732.23	1732.97	-0.74	43-57		
	5 PEAKS MATCH WITH BMP-3	HUMAN	4557371 (NCBI)	1060.43	1060.20	0.23	102-111	31	% COVERAGE CALCULATION IS RELATIVE TO THE MATURE BMP-3, 183 AAS (290-472)
				1438.83	1438.58	0.25	346-357		
				1566.92	1566.76	0.16	345-357		
				1651.80	1651.91	-0.11	410-424		
				3408.86	3407.77	1.09	290-318		

FIG.16E

IDENTIFICATION OF PROTEINS BY MASS SPECTROMETRY OF TRYPTIC FRAGMENTS FROM 1D GELS

BAND	MASS SPEC PROFILE	SPECIES	ACC. NO.	MASS SPEC DATA	MASS SPEC DATABASE	MASS DIFFERENCE	AAs	% COVERAGE	COMMENTS
29	4 PEAKS MATCH WITH BMP-3	HUMAN	4557371 (NCBI)	1113.22	1113.31	-0.09	361-368	27	% COVERAGE CALCULATION IS RELATIVE TO THE MATURE BMP-3, 183 AAs (290-472)
				1438.70	1438.58	0.12	346-357		
				1566.86	1566.75	0.11	345-357		
				3409.04	3407.77	1.27	290-318		

FIG.16F

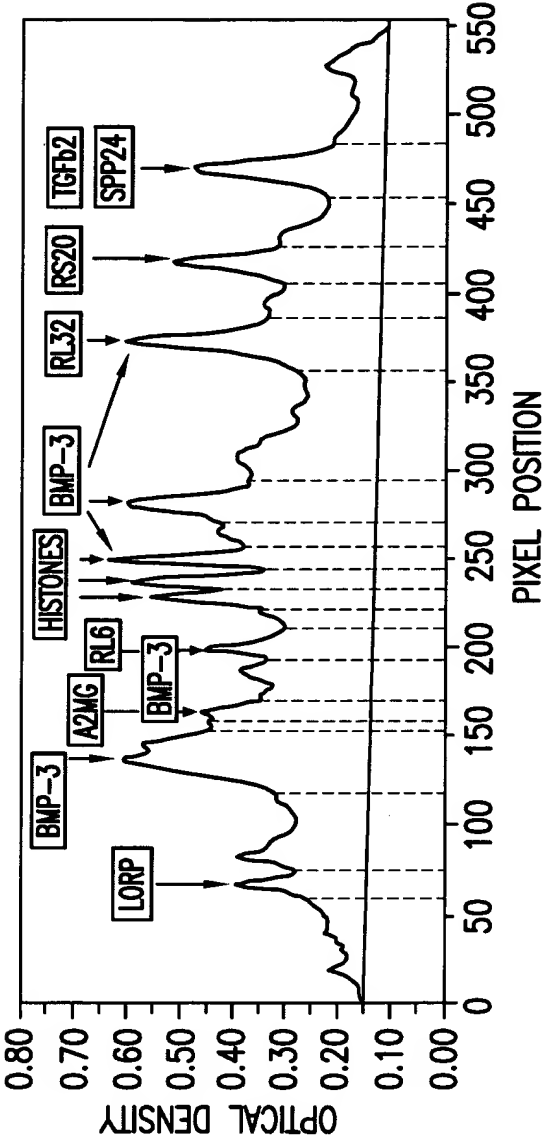


FIG.17A

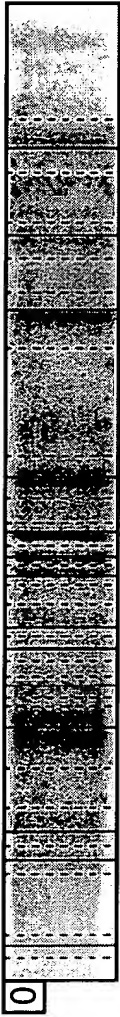


FIG.17B

QUANTITATION OF IDENTIFIED BP PROTEINS

IDENTIFIED PROTEIN	PERCENTAGE OF TOTAL PROTEIN
LORP	2
BMP-3	11
BMP-3 AND A2-MG	3
RL6 & BMP-3	4
HISTONE	3
HISTONE	3
HISTONE & BMP-3	4
BMP-3	8
RL32 & BMP-3	8
RS2D	5
SPP24 & TGF- β 2	6
TOTAL	58%

FIG.18

IDENTIFICATION OF PROTEINS BY MASS SPECTROMETRY OF FRAGMENTS FROM 2D GELS

BAND	DIGEST	MASS SPEC PROFILE	SPECIES	ACC. NO.	MS PEAKS			AAs	% COVERAGE	COMMENTS
					DATA	DATABASE	DIFF			
1	Lys-C	2 PEAKS MATCH WITH COAGULATION FACTOR XIIIb	HUMAN	P05160 (SWISS-PROT)	1837.01	1837.14	-0.13	472-487	8	PEPTIDE MATCH CONFIRMED BY SEQUENCE ANALYSIS
					1921.65	1921.14	0.51	366-382		
					2679.51	N/A	N/A	488-504		
2	TRYPSIN	2 PEAKS MATCH WITH LORP	HUMAN	NP002309 (SWISS-PROT)	1609.57	1609.88	-0.31	241-253	5	
					2410.89	2410.63	0.26	648-669		
3	Lys-C	8 PEAKS MATCH WITH CATHEPSIN L PRECURSOR	BOVINE	P25975 (SWISS-PROT)	1407.26	1406.80	0.46	105-116	41	
					1546.84	1546.70	0.14	58-70		
					1661.16	1660.80	0.36	21-33		
					1681.86	1680.80	1.06	301-314		
					1834.71	1834.00	0.71	318-334		
					2352.90	2351.50	1.40	274-295		
					2381.50	2380.70	0.80	239-261		
					2721.51	2721.10	-0.41	131-154		

FIG.19A

IDENTIFICATION OF PROTEINS BY MASS SPECTROMETRY OF FRAGMENTS FROM 2D CELS

SPOT	DIGEST	MASS SPEC PROFILE	SPECIES	ACC. NO.	MS PEAKS			AAs	% COVERAGE	COMMENTS
					DATA	DATABASE	DIFF			
4	Lys-C	2 PEAKS MATCH WITH LYSYL OXIDASE	RAT	P16636 (SWISS-PROT)	1461.58	N/A	N/A			PEPTIDE MATCHES CONFIRMED BY SEQUENCE ANALYSIS
					4595.08	4593.06	2.02			
5	Lys-C	3 PEAKS MATCH WITH TGF-b2	BOVINE	P21214 (SWISS-PROT)	774.56	774.90	-0.34	26-31	20	
					809.67	809.94	-0.27	32-37		
					1175.26	1175.43	-0.17	98-107		
					1415.56	1415.58	-0.02	42-60	16	
2	TRYPSIN	13 PEAKS MATCH WITH SPP24	BOVINE	Q27967 (SWISS-PROT)	2187.98	2187.51	0.47	21-32		
					1078.06	1078.15	-0.09	78-85	60	
					1101.07	1101.31	-0.24	99-108		
					1172.42	1172.31	0.11	99-108		
					1411.53	1411.60	-0.07	42-53		
					1447.63	1447.65	-0.02	113-124		
					1540.57	1540.52	0.05	86-98		
					1696.79	1696.71	0.08	85-98		
					1869.16	1869.05	0.11	62-77		
					2026.01	2025.24	0.77	61-77		
					2272.97	2272.56	0.41	21-41		
					2600.18	2599.65	0.53	78-98		
					2693.30	2693.81	-0.51	86-108		
					2928.80	2928.01	0.79	125-151		

FIG.19B

IDENTIFICATION OF PROTEINS BY MASS SPECTROMETRY OF FRAGMENTS FROM 2D GELS

SPOT	DIGEST	MASS SPEC PROFILE	SPECIES	ACC. NO.	MS PEAKS			AAs	% COVERAGE	COMMENTS
					DATA	DATABASE	DIFF			
7	Lys-C	4 PEAKS MATCH WITH TGF- β 2	BOVINE	P21214 (SWISS-PROT)	774.56	774.90	-0.34	26-31	42	
					809.69	809.94	-0.25	32-37		
					1175.12	1175.43	-0.31	98-107		
					3168.10	3166.66	1.44	1-25		
					2187.77	2187.51	0.26	42-60	10	
8	TRYPSIN	12 PEAKS MATCH RIBOSOME L3	BOVINE	P39872 (SWISS-PROT)	917.39	917.14	0.25	348-355	37	
					984.23	984.15	0.08	10-18		
					1192.62	1192.40	0.22	286-296		
					1380.67	1380.65	0.02	249-260		
					1464.80	1464.63	0.17	103-114		
					1620.86	1620.82	0.04	103-115		
					1778.84	1779.00	-0.16	34-49		
					2238.43	2238.55	-0.12	30-49		
					2325.99	2325.65	0.34	177-197		
					2661.31	2661.04	0.27	200-223		
					2897.94	2898.43	-0.49	70-98		
					2946.10	2946.35	-0.25	198-223		

FIG.19C

IDENTIFICATION OF PROTEINS BY MASS SPECTROMETRY OF FRAGMENTS FROM 2D GELS

SPOT	DIGEST	MASS SPEC PROFILE	SPECIES	ACC. NO.	MS PEAKS			AAS	% COVERAGE	COMMENTS
					DATA	DATABASE	DIFF			
9	TRYPSIN	7 PEAKS MATCH WITH RIBOSOME S3a	MOUSE	P97351 (SWISS-PROT)	920.05	920.10	-0.05	19-26	29	
					1218.29	1218.31	-0.02	152-161		
					1346.62	1346.49	0.13	151-161		
					1516.69	1516.69	0.00	174-186		
					1593.72	1593.82	-0.10	94-106		
					1719.91	1720.00	-0.09	199-212		
					1953.12	1953.16	-0.04	65-81		
10	TRYPSIN	4 PEAKS MATCH WITH HISTONE H1.c	HUMAN	87668 (NCBI)	1327.75	1327.56	0.19	34-46	23	
					1579.70	1579.71	-0.01	65-79		
					1707.65	1707.89	-0.24	64-79		
					2147.17	2147.53	-0.36	1-21		
					1168.48	1168.38	0.10	230-239		
11	TRYPSIN	6 PEAKS MATCH WITH RIBOSOME S4	HUMAN	P12750 (SWISS-PROT)	1216.39	1216.39	0.00	134-144	23	
					1354.03	1353.61	0.42	230-241		
					1507.81	1507.89	0.12	198-210		
					1557.75	1557.98	-0.23	37-48		
					2140.34	2140.58	-0.24	221-239		
					2591.80	2591.90	-0.10	77-99		

FIG.19D

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